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(54) Title: VIRULENCE GENES, PROTEINS, AND THEIR USE

(57) Abstract: A series of genes from *Pseudomonas aeruginosa* and *Klebsiella* are shown to encode products that are implicated in virulence. The identification of theses genes therefore allows attenuated microorganisms to be produced. Furthermore, the genes or their encoded products can be used to identify antimicrobial drugs, diagnostic methods for the identification of a pathogen-associated disease, and in the manufacture of vaccines.

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VIRULENCE GENES, PROTEINS, AND THEIR USE

FIELD OF THE INVENTION

This invention relates to virulence genes and proteins, and their use. More particularly, it relates to genes and proteins/peptides obtained from gram-negative bacteria, and their use in therapy and in screening for drugs.

BACKGROUND OF THE INVENTION

According to health care experts, infectious diseases caused by microbes are responsible for more deaths worldwide than any other single cause. The current estimate of the annual cost of medical care for treating infectious diseases in the United States alone is about $120 billion. While antibiotic treatment is effective for many microbial infections, antibiotic resistance among pathogenic bacteria is a growing health concern. Indeed, the American Medical Association has concluded that, "the global increase in resistance to antimicrobial drugs, including the emergence of bacterial strains that are resistant to all available antibacterial agents, has created a public health problem of potentially crisis proportions."

Pseudomonas and *Klebsiella* are two genuses of gram-negative bacteria that pose a significant health risk to infected host organisms, in part, due to their resistance to many antibiotics. These bacteria are noted for causing life-threatening infections, particularly in the lung. Cancer and burn patients also commonly suffer serious *Pseudomonas* infections, as do certain other individuals with immune system deficiencies. While *Klebsiella* sp. is responsible for many types of infections, outside of a medical setting, the most common infection caused by *Klebsiella* bacteria is pneumonia.

There is a need in the art for new antimicrobial therapeutic strategies.

SUMMARY OF THE INVENTION

The present invention is based, in part, on the discovery of 46 genes, when mutated lower the virulence of a gram-negative bacterium, and can be used in new antimicrobial therapeutic strategies. The invention provides attenuated bacterial mutants that are derived from pathogenic strains. These attenuated bacterial stains have a mutation in a VIRX gene identified herein as VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and show reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain. The term, "pathogenic," as used herein, is defined as an agent's ability to cause disease, damage or harm to a host organism. The term, "attenuated," as used herein, means an organism made less virulent relative to an isogenic pathogenic organism. The term, "mutant," as used herein, an organism carrying a specific mutation of a gene that is expressed in the organism's phenotype. A mutation may be insertional inactivation or deletion of a gene. It is preferred that the mutation be an insertional inactivation of a gene.

The invention also provides attenuated bacterial mutants that are derived from pathogenic gram-negative bacterial strains. These attenuated gram-negative bacterial strains have a mutation in a VIRX gene identified herein as VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and show reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain. A mutation may be insertional inactivation or deletion of a gene. It is preferred that the mutation be an insertional inactivation of a gene. It is also preferred that the attenuated gram-negative bacterial mutant be derived from a *Pseudomonas* or *Klebiella* spp. It is more preferred that the attenuated gram-negative bacterial mutant is a strain of *P. aeruginosa* or *K. pneumoniae*.

The invention additionally provides for a VIRX gene that may be part of an operon. The term, "operon," as used herein, is a unit of bacterial gene expression and regulation

comprising several genes, usually with complementary functions. Insertion in a gene in an operon typically interferes with the function of this gene and of other genes located downstream or upstream in the operon. The function attributed to a gene refers to its function and/or that of any gene located downstream or upstream in the same operon. Accordingly, the invention also provides for a bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein the bacterial strain includes a mutation that reduces expression of the VIRX gene relative to an isogenic bacterial strain lacking the mutation. In one embodiment, the the mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking the mutation.

The invention provides for one or more of the following attenuated *Pseudomonas* mutant strains: MUT1; MUT2; MUT3; MUT4; MUT5; MUT6; MUT7; MUT8; MUT9; MUT10; MUT11; MUT12; MUT13; MUT14; MUT15; MUT16; MUT17; MUT18; and MUT19. The invention also provides for one or more of the following attenuated *Klebsiella* mutant strains: MUT20; MUT21; MUT22; MUT23; MUT24; MUT25; MUT26; MUT27; MUT28; MUT29; MUT30; MUT31; MUT32; MUT33; MUT34; MUT35; MUT36; MUT37; MUT38; MUT39; MUT40; MUT41; MUT42; MUT43; MUT44; MUT45; and MUT46.

The invention additionally provides a method for identifying an antimicrobial drug, wherein a candidate composition is contacted with at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45 and VIR46. The biological activity of polypeptide in the presence of the candidate composition is compared with the biological activity of the polypeptide in the absence of the candidate composition. Alteration of the biological activity of the polypeptide indicates that the candidate composition is an antimicrobial drug. In some embodiments, the candidate composition contains at least two molecules. The candidate

composition can contain at least one molecule less than about 500 Daltons or at least one molecule greater than about 500 Daltons. The candidate composition can be, *e.g.*, an immunoglobulin, polysaccharide, lipid, nucleic acid, or combination thereof.

The invention additionally provides a method for identifying an antimicrobial drug, wherein a candidate composition is contacted with at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46. The expression of the polynucleotide in the presence of the candidate composition is compared with the expression of the polynucleotide in the absence of the candidate composition. Alteration of the expression of the polynucleotide indicates that the candidate composition is an antimicrobial drug. In some embodiments, the candidate composition contains at least two molecules. The candidate composition can contain at least one molecule less than about 500 Daltons or at least one molecule greater than about 500 Daltons. The candidate composition can be a polypeptide, polysaccharide, lipid, nucleic acid, *e.g.*, ribonucleic acid, or combination thereof. In a preferred embodiment, the ribonucleic acid of the candidate composition is a small interfering ribonucleic acid.

The invention additionally provides a method for determining the degree of virulence of a pathogen present in a subject, comprising:

(a) measuring the level of expression of at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of the polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second subject known not to have the presence of the pathogen, wherein an alteration in the

expression level of the polypeptide in the first subject as compared to the control sample indicates the degree of virulence of the pathogen.

In a preferred embodiment, the subject is a mammal. It is more preferred that the subject is a human.

The invention also provides a method for determining the degree of virulence of a pathogen present in a subject, comprising:

(a) measuring the level of expression of at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of the polynucleotide in the sample of step (a) to the amount of the polynucleotide present in a control sample from a second subject known not to have the presence of the pathogen, wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the degree of virulence of the pathogen.

In a preferred embodiment, the subject is a mammal. It is more preferred that the subject is a human.

The invention additionally provides attenuated bacterial strains that can be used as vaccines and as vectors for foreign antigens and for foreign DNA. These attenuated bacterial strains are useful for the preparation of vaccines effective against diseases associated with the corresponding bacterial strains. In a preferred embodiment, the attenuated bacterial strains are derived from *Pseudomonas* or *Klebsiella* spp.

The invention additionally provides attenuated bacterial strains that can be used as vectors for foreign genes cloned from other pathogens that will be expressed into proteins, and will raise protective immune responses against the pathogens from which they are derived. In a preferred embodiment, the attenuated bacterial strains used as the vectors are derived from *Pseudomonas* or *Klebsiella* spp.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based , in part, on the discovery of 46 genes when mutated lower the virulence of a gram-negative bacterium. Nineteen of these virulence genes were identified in *P. aeruginosa* PT894, while the remaining 27 genes were derived from mutagenesis of *Klebsiella*. These bacterial mutants have attenuated virulence relative to isogenic bacterial strains and are designated "MUTX." Provided herein are virulence genes affected in each novel, attenuated MUTX strain, as well as the nucleotides and polypeptides encoded thereby. The sequences encoded by the affected genes are collectively referred to as "VIRX nucleic acids" or "VIRX polynucleotides" and the corresponding encoded polypeptides are referred to as "VIRX polypeptides" or "VIRX proteins." Unless indicated otherwise, "VIRX" is meant to refer to any of the novel sequences disclosed herein.

The peptides and genes of the invention are useful for the preparation of therapeutic agents to treat infection because they attenuate the virulence of the wild-type pathogen. Therapy can be preventative or therapeutic. A subject receiving therapy can be, *e.g.*, a human, a non-human primate (such as an ape, gorilla, or chimpanzee), cow, horse, pig, sheep, dog, cat, or rodent (including mouse or rat).

I. IDENTIFICATION OF *PSEUDOMONAS* AND *KLEBSIELLA* GENES ENCODING VIRULENCE FACTORS

Genes encoding virulence factors (*e.g.*, pathogens or toxins) to a host organism were

identified by comparing the growth of *Dictyostelium discoideum*, in the presence and absence of test mutants of *Pseudomonas* and *Klebsiella* with an identifiable genetic alteration as detailed in International Application PCT/IB02/03277, filed June 7, 2002. *Dictyostelium* amoebae feed phagocytically upon bacteria such as *K. pneumoniae*. When *Dictyostelium* cells are plated with *K. pneumoniae* bacteria, each amoeba creates a plaque in the bacterial lawn in the region where bacteria have been phagocytosed. Addition of pathogenic bacteria, *e.g.*, *P. aeruginosa* strain *PT894* to the lawn of *K. pneumoniae* bacteria, inhibits the growth of the amoebae.

Pseudomonas test mutants were made by transposon insertion according to known methods in the art and tested for virulence in a *Dictyostelium* growth assay (*see*, PCT/IB02/03277, filed June 7, 2002). *Klebsiella* mutants were also made by transposon insertion according to known methods in the art and tested for virulence in a *Dictyostelium* growth assay (*see*, PCT/IB02/03277, filed June 7, 2002) using the *PHG1a* mutant *Dictyostelium* strain (Cornillon *et al.*, J. Biol. Chem., 275(44): 34287-92, 2000), a strain which was found to be particularly sensitive to virulent bacteria. Specifically, the *Klebsiella* mutants were obtained by standard bacteria electroporation technique using the plasposon pNKBOR (Genbank accession number: AF310136) and selected on solid LB medium containing 50 µg/ml kanamycin (Rossignol *et al.*, Res. Microbiol., 152(5): 481-5, 2001). Other mutagenesis methods known in the art, *e.g.*, ultraviolet radiation exposure, treatment with intercalating agent or transducing phage, may also be used to generate mutants. Mutations yielding reduced virulence were identified where the growth of the *Dictyostelium* test host organism exposed to the mutant pathogen was greater than the *Dictyostelium* test host organism exposed to wild-type pathogen. Specific genetic mutations in pathogens displaying reduced virulence were subsequently identified and characterized by techniques well known in the art. Identification of specific gene mutations in *Klebsiella* mutants was performed by plasmid rescue and cloning of the genomic DNA at the insertion site mutant using the BglII or ApaI restriction enzyme according to (Rossignol *et al.*, Res. Microbiol., 152(5): 481-5, 2001). Identification of specific gene mutations in *Pseudomonas* mutants was performed by subcloning the transposon and surrounding bacteria genomic DNA into an acceptor plamid. DNA sequencing was performed on amplified rescued plasmids, in order to identify the insertion site of the transposon. Rat mortality assays such as that described by Join-Lambert *et al.*, Antimicrob. Agents Chemother., 45(2): 571-6, 2001, can be used to

corroborate attenuated virulence activity in a mammalian host.

The 19 *Pseudomonas* attenuated MUTX organisms harboring the VIRX genes are summarized below in Table 1.

Table 1

STRAIN	AFFECTED VIRULENCE GENE(S)	REFERENCE
MUT1	anthranilate phosphoribosyltransferase (trpD; PA0650)	Essar *et al.*, J. Bacteriol., 172:853-66, 1990; Essar *et al.*, J. Bacteriol., 172:867-83,1990.
MUT2	ATP sulfurylase small subunit (CysD; PA4443)	Leyh *et al.*, J. Biol. Chem., 263:2409-16,1988; Hummerjohann *et al.*, Microbiology, 144 (Pt 5):1375-86, 1998
MUT3	CysQ (PA5175)	Peng and Verma, J. Biol. Chem., 270:29105-10, 1995; Neuwald *et al.*, J. Bacteriol., 174:415-25, 1992.
MUT4	D-amino acid dehydrogenase, small subunit (dadA; PA5304)	Lobacka *et al.*, J. Bacteriol., 176:1500-10, 1994.
MUT5	imidazoleglycerol-phosphate synthase, cyclase subunit (hisF1; PA5140)	Fani *et al.*, Mol. Gen. Genet., 216:224-9, 1989; Fani *et al.*, Mol. Gen. Genet., 216:224-9, 1989.
MUT6	N-acetyl-γ -glutamyl-phosphate reductase (ArgC; PAO 0662)	Smith *et al.*, Gene, 49:53-60, 1986.
MUT7	Dihydrolipoamide acetyltransferase (AceF; pyruvate dehydrogenase complex component E2; PA5016)	Rae *et al.*, J. Bacteriol., 179:3561-71, 1997.
MUT8	NADH dehydrogenase I chain H (nuoH; PA2643)	Weidner *et al.*, J. Mol. Biol., 5:233:109-22, 1993; Weidner *et al.*, J. Mol. Biol., 233:109-22, 1993.
MUT9	pyoverdine synthetase D (PvdD; PA2399)	Rombel *et al.*, Mol. Gen. Genet., 246:519-28, 1995; Merriman *et al.*, J. Bacteriol., 177:252-8, 1995.
MUT10	RND multidrug efflux transporter MexD (mexD;PA4598)	Poole *et al.*, Mol. Microbiol., 21:713-24, 1996; Poole *et al.*, Mol. Microbiol., 21:713-24, 1996.
MUT11	PA3721	Stover *et al.*, Nature, 406:959-964, 2000.
MUT12	PA0596	Tan *et al.*, Proc. Natl. Acad. Sci. USA, 96:2408-13, 1999.
MUT13	PA5265	Stover *et al.*, Nature, 406: 959-964, 2000.

MUT14	pyochelin biosynthetic protein pchC (PA4229)	Serino *et al.*, Mol. Gen. Genet., 249: 217-28, 1995; Serino *et al.*, J. Bactiol., 179:248-57, 1997
MUT15	dihydroaeruginoic acid synthetase (pchE; PA4226)	Reimmann *et al.*, Microbiology, 144: 3135-48, 1998.
MUT16	Pyochelin synthetase (pchF; PA4225)	Reimmann *et al.*, Microbiology, 144: 3135-48, 1998.
MUT17	ATP-binding component of the ABC transporter (pchH; PA4223)	Featherston *et al.*, Mol. Microbiol., 32(2):289-99, 1999; Reimmann *et al.*, J. Bacteriol., 183:813-20, 2001.
MUT18	ATP-binding component of the ABC transporter (pchI; PA4222)	Reimmann *et al.*, J. Bacteriol., 183:813-20, 2001.
MUT19	putative O-antigen biosynthesis gene cluster	Rocchetta *et al.*, Microbiol. Mol. Biol. Rev. 63:523-53, 1999.

The 27 *Klebsiella* attenuated MUTX organisms harboring the VIRX genes disclosed in the present invention and assigned a new role in virulence are summarized below in Table 2.

Table 2

STRAIN	AFFECTED VIRULENCE GENE(S)
MUT20	hypothetical transcriptional regulator in met G-dld intergenic region
MUT21	β-cystathionase
MUT22	ribosome binding factor A
MUT23	aspartokinase/homoserine dehydrogenase
MUT24	cystathionine γ-synthase
MUT25	Phophoribosylformylglycinamidine synthase

MUT26	homoserine transsuccinylase
MUT27	3'-phosphoadenosine 5'-phosphosulfate reductase
MUT28	Sfi protein
MUT29	transcriptional activator protein LysR
MUT30	TrpD
MUT31	N-acetylglucosamine-6-phosphate deacetylase
MUT32	WaaQ
MUT33	2-Isopropylmalate synthase
MUT34	histidinol dehydrogenase
MUT35	UDP-galactopyranose mutase
MUT36	O-antigen export system permease protein rfba
MUT37	uridyltransferase
MUT38	pyridoxine phosphate biosynthetic protein PdxJ-PdxA
MUT39	triose phosphate isomerase
MUT40	aldehyde dehydrogenase
MUT41	galactosyl transferase
MUT42	siroheme synthetase
MUT43	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase
MUT44	glucose-6-phosphate isomerase
MUT45	DNA methylase
MUT46	putative inner membrane protein

II. ATTENUATED BACTERIAL MUTANTS

A. Attenuated *Pseudomonas aeruginosa* Mutants

MUT1

A *Pseudomonas* bacterial mutant (MUT1) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding anthranilate phosphoribosyltransferase (PA0650). This gene encodes the VIR1 nucleic acid (SEQ ID NO:1) shown in Table 3A.

Table 3A. VIR1 Nucleotide Sequence (SEQ ID NO:1)

```
ATGGATATCAAGGGAGCCCTCAATCGCATCGTCAACCAGCTCGACCTGACCACCGAGGAAATGCAGG
CGGTCATGCGCCAGATCATGACCGGGCAGTGCACCGACGCGCAGATCGGCGCCTTCCTGATGGGCAT
GCGGATGAAGAGCGAAACCATCGACGAGATCGTCGGCGCGGTGGCGGTGATGCGCGAACTGGCCGAC
GGCGTGCAGTTGCCTACGCTGAAGCATGTGGTCGACGTGGTCGGCACCGGCGGCGATGGCGCGAACA
TCTTCAACGTGTCCTCGGCGGCGTCCTTCGTGGTCGCCGCCGCTGGCGGCAAGGTCGCCAAACACGG
TAACCGCGCGGTCTCCGGCAAGAGCGGCAGCGCCGACTTGCTGGAAGCCGCCGGCATCTACCTGGAG
CTGACCTCCGAACAGGTGGCGCGTTGCATCGACACCGTCGGCGTCGGGTTCATGTTCGCCCAGGTCC
ACCACAAGGCGATGAAGTACGCCGCCGGTCCGCGCCGCGAGCTGGGCTTGCGGACTCTGTTCAACAT
GCTTGGCCCACTGACCAACCCGGCGGGAGTCAGGCACCAGGTGGTCGGGGTGTTCACCCAGGAACTG
TGCAAGCCGCTGGCTGAAGTGCTCAAGCGTCTCGGCAGCGAGCATGTGCTGGTGGTGCATTCGCGCG
ACGGGCTGGACGAGTTCAGTCTGGCCGCGGCGACCCACATTGCCGAGTTGAAGGACGGCGAGGTACG
CGAGTACGAAGTGCGTCCCGAGGACTTCGGGATCAAGAGCCAGACCCTGATGGGGCTGGAGGTCGAC
AGTCCGCAGGCCTCGCTGGAACTGATCCGCGACGCTTTGGGGCGGCGCAAGACCGAGGCTGGGCAGA
AGGCCGCCGAGCTGATCGTGATGAATGCCGGCCCGGCACTGTACGCTGCCGATCTGGCGACCAGCCT
GCACGAGGGCATTCAACTGGCCCACGATGCCCTGCACACCGGGCTGGCACGGGAGAAGATGGACGAA
CTGGTGGCCTTCACCGCCGTTTACAGAGAGGAGAACGCACAGTGA
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The VIR1 protein (SEQ ID NO:2) encoded by SEQ ID NO:1 is presented using the one-letter amino acid code in Table 3B.

Table 3B. Encoded VIR1 protein sequence (SEQ ID NO:2)

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MDIKGALNRIVNQLDLTTEEMQAVMRQIMTGQCTDAQIGAFLMGMRMKSETIDEIVGAVAVMREL
ADGVQLPTLKHVVDVVGTGGDGANIFNVSSAASFVVAAAGGKVAKHGNRAVSGKSGSADLLEAAG
IYLELTSEQVARCIDTVGVGFMFAQVHHKAMKYAAGPRRELGLRTLFNMLGPLTNPAGVRHQVVG
VFTQELCKPLAEVLKRLGSEHVLVVHSRDGLDEFSLAAATHIAELKDGEVREYEVRPEDFGIKSQ
TLMGLEVDSPQASLELIRDALGRRKTEAGQKAAELIVMNAGPALYAADLATSLHEGIQLAHDALH
TGLAREKMDELVAFTAVYREENAQ
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The role of VIR1 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT2

A *Pseudomonas* bacterial mutant (MUT2) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the ATP sulfurylase small subunit (CysD; PA4443). This gene encodes the VIR2 nucleic acid (SEQ ID NO:3) shown in Table 4A.

Table 4A. VIR2 Nucleotide Sequence (SEQ ID NO:3)

```
ATGGTCGACAAACTGACGCACCTGAAACAGCTGGAGGCGGAAAGCATCCACATCATCCGCGAGGTGG
CCGCCGAGTTCGATAACCCGGTGATGCTGTACTCGATCGGCAAGGATTCCGCGGTCATGCTGCACCT
GGCCCGCAAGGCCTTCTTCCCCGGCAAGCTGCCCTTCCCGGTGATGCACGTGGACACCCGCTGGAAA
TTCCAGGAGATGTACAGGTTCCGTGATCGGATGGTCGAGGAAATGGGCCTGGATCTGATCACCCACG
TCAACCCGGACGGCGTCGCCCAGGGCATCAACCCGTTCACCCACGGCAGCGCCAAGCACACCGACGT
GATGAAGACCGAGGGACTCAAGCAGGCCCTGGACAAGTACGGTTTCGACGCTGCCTTCGGCGGTGCG
CGCCGCGACGAGGAGAAGTCGCGGGCCAAGGAACGGGTCTATTCGTTCCGCGACAGCAAGCACCGCT
GGGACCCGAAGAACCAGCGTCCCGAGCTGTGGAACATCTACAACGGCAAGGTGAAGAAGGGCGAGTC
GATCCGCGTCTTCCCGCTGTCCAACTGGACCGAGCTGGACATCTGGCAATACATCTACCTGGAAGGC
ATCCCGATCGTCCCGCTGTACTTCGCCGCCGAGCGCGAGGTCATCGAGAAGAATGGCACATTGATCA
TGATCGACGACGAGCGCATCCTCGAGCATCTCTCTGACGAAGAGAAAGCCCGCATCGAGAAGCGCAT
GGTGCGCTTCCGTACCCTCGGCTGCTACCCGCTCACCGGCGCGGTCGAGTCCAGCGCCACCACGCTG
CCGGAAATCATCCAGGAAATGCTCCTGACGCGTACTTCCGAACGCCAGGGCCGGGTCATCGACCATG
ACCAGGCCGGTTCGATGGAAGAAAAGAAACGTCAGGGCTATTTCTGA
```

The VIR2 protein (SEQ ID NO:4) encoded by SEQ ID NO:3 is presented using the one-letter amino acid code in Table 4B.

Table 4B. Encoded VIR2 protein sequence (SEQ ID NO:4)

```
MVDKLTHLKQLEAESIHIIREVAAEFDNPVMLYSIGKDSAVMLHLARKAFFPGKLPFPVMHVDTR
WKFQEMYRFRDRMVEEMGLDLITHVNPDGVAQGINPFTHGSAKHTDVMKTEGLKQALDKYGFDAA
FGGARRDEEKSRAKERVYSFRDSKHRWDPKNQRPELWNIYNGKVKKGESIRVFPLSNWTELDIWQ
YIYLEGIPIVPLYFAAEREVIEKNGTLIMIDDERILEHLSDEEKARIEKRMVRFRTLGCYPLTGA
VESSATTLPEIIQEMLLTRTSERQGRVIDHDQAGSMEEKKRQGYF
```

The role of VIR2 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT3

A *Pseudomonas* bacterial mutant (MUT3) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding CysQ (PA5175). This gene encodes the VIR3 nucleic acid (SEQ ID NO:5) shown in Table 5A.

Table 5A. VIR3 Nucleotide Sequence (SEQ ID NO:5)

```
ATGAGGCCGGTGCCTTGGGGCGAATTGGTGGCGCTGGTGCGGCGCGCCGGCGAGGCGATCCTGCCGC
ACTGGCGCGCCGACGTGGTGGTGCGCTCGAAGGCCGACGAATCGCCGGTGACTGCCGCCGACCTGGC
CGCGCACCATATATTGGAGGCGGGATTGCGGGCGCTGGCGCCGGACATTCCGGTGCTTTCCGAAGAG
GATTGCGAGATACCGCTGAGCGAGCGCGGCCACTGGCGGCGCTGGTGGCTGGTGGACCCGCTGGACG
GCACCAAGGAGTTCATCTCCGGTAGCGAGGAGTTCACCGTCAACGTGGCCCTGGTCGAGGATGGCCG
GGTGCTGTTCGGCCTGGTCGGCGTGCCGGTGAGCGGCCGCTGCTACTACGGTGGCGCCGGTCTCGGT
GCCTGGCGCGAGGAGGCCGATGGCCGCGCGCAACCGATCAGTGTGCGCCTGGAGCCCGAGGAGGCCT
TCACCGTGGTGGCCAGCAAGCGCCATGGCAGCCCGGCCCAGGAGCGCCTGCTGGATGGCTTGAGCGA
GCGCTTCGGCGACCTGCGGCGAGCCAGCATCGGCAGTTCGCTGAAGTTCTGCCTGCTGGCCGAGGGC
GCTGCCGACTGCTATCCGCGCCTGACGCCAACCTCGCAATGGGACACGGCCGCCGCCCAGGGTGTGC
TGGAAGGCGCCGGCGGCGAGGTGCTCGACCTGCATGGTGCGCCATTCACCTACGAGCCGCGCGAGGA
TTACCTCAACGGCTCCTTCCTGGCCCTGCCGCGCGCCGCCGAGTGGCGCAGCGAGCTGATCCAACTG
GCGCGCGCGCTGCACTGA
```

The VIR3 protein (SEQ ID NO:6) encoded by SEQ ID NO:5 is presented using the one-letter amino acid code in Table 5B.

Table 5B. Encoded VIR3 protein sequence (SEQ ID NO:6)

```
MRPVPWGELVALVRRAGEAILPHWRADVVVRSKADESPVTAADLAAHHILEAGLRALAPDIPVLS
EEDCEIPLSERGHWRRWWLVDPLDGTKEFISGSEEFTVNVALVEDGRVLFGLVGVPVSGRCYYGG
AGLGAWREEADGRAQPISVRLEPEEAFTVVASKRHGSPAQERLLDGLSERFGDLRRASIGSSLKF
CLLAEGAADCYPRLTPTSQWDTAAAQGVLEGAGGEVLDLHGAPFTYEPREDYLNGSFLALPRAAE
WRSELIQLARALH
```

MUT4

A *Pseudomonas* bacterial mutant (MUT4) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding D-amino acid dehydrogenase, small subunit (dadA; PA5304). This gene encodes the VIR4 nucleic acid (SEQ ID NO:7) shown in Table 6A.

Table 6A. VIR4 Nucleotide Sequence (SEQ ID NO:7)

```
ATGCGAGTTCTGGTCCTTGGCAGCGGTGTCATCGGTACCGCCAGTGCGTATTACCTGGCCCGTGCCG
GGTTCGAGGTGGTGGTGGTCGACCGTCAGGACGGTCCCGCGCTGGAAACCAGCTTCGCCAACGCCGG
```

CCAGGTGTCTCCCGGCTACGCTTCGCCCTGGGCAGCCCCGGGCATTCCCCTGAAGGCCATGAAGTGG
CTGCTGGAAAAGCACGCGCCGCTGGCCATCAAGCTCACCTCCGATCCCAGCCAGTACGCCTGGATGC
TGCAGATGCTGCGCAACTGCACCGCCGAGCGCTACGCCGTGAACAAGGAGCGCATGGTCCGCCTGTC
CGAGTACAGCCGCGATTGCCTCGACGAACTGCGCGCCGAGACCGGCATCGCCTACGAGGGCCGCACC
CTCGGCACCACCCAACTGTTCCGCACCCAGGCGCAGCTGGACGCCGCCGGCAAGGACATCGCCGTGC
TCGAGCGCTCCGGCGTGCCCTACGAGGTTCTCGACCGCGACGGCATCGCCCGCGTAGAGCCGGCTTT
GGCCAAGGTCGCCGACAAGCTGGTCGGCGCCTTGCGCCTGCCCAACGACCAGACCGGCGACTGCCAG
CTGTTCACCACCCGCCTGGCGGAAATGGCCAAGGGCCTGGGCGTGGAGTTCCGCTTCGGCCAGAACA
TCGAGCGCCTGGACTTCGCCGGCGACCGCATCAACGGCGTGCTGGTCAACGGCGAATTGCTCACCGC
CGACCACTACGTGCTGGCCCTGGGCAGCTACTCGCCGCAACTGCTCAAGCCGCTGGGTATCAAGGCT
CCGGTCTATCCGCTGAAGGGTTATTCGCTGACCGTGCCGATCACCAACCCGGAGATGGCGCCGACCT
CGACCATCCTCGACGAGACCTACAAGGTGGCGATCACCCGCTTCGACCAGCGCATCCGCGTCGGCGG
CATGGCGGAAATCGCCGGCTTCGACCTGTCGCTGAACCCGCGCCGCCGCGAGACCCTGGAAATGATC
ACCACCGACCTCTATCCCGAGGGCGGCGATATCAGCCAGGCGACCTTCTGGACCGGCCTGCGCCCGG
CGACCCCGGATGGCACCCCGATCGTCGGCGCCACCCGCTACCGCAACCTGTTCCTCAATACCGGCCA
CGGCACCCTGGGTTGGACCATGGCCTGCGGGTCGGGTCGCTACCTGGCCGACCTGATGGCGAAGAAG
CGCCCGCAGATCAGTACCGAAGGCCTGGATATTTCCCGCTACAGCAATTCCCCGGAGAACGCCAAGA
ATGCCCATCCAGCGCCAGCACACTAA

The VIR4 protein (SEQ ID NO:8) encoded by SEQ ID NO:7 is presented using the one-letter amino acid code in Table 6B.

Table 6B. Encoded VIR4 protein sequence (SEQ ID NO:8)

MRVLVLGSGVIGTASAYYLARAGFEVVVVDRQDGPALETSFANAGQVSPGYASPWAAPGIPLKAM
KWLLEKHAPLAIKLTSDPSQYAWMLQMLRNCTAERYAVNKERMVRLSEYSRDCLDELRAETGIAY
EGRTLGTTQLFRTQAQLDAAGKDIAVLERSGVPYEVLDRDGIARVEPALAKVADKLVGALRLPND
QTGDCQLFTTRLAEMAKGLGVEFRFGQNIERLDFAGDRINGVLVNGELLTADHYVLALGSYSPQL
LKPLGIKAPVYPLKGYSLTVPITNPEMAPTSTILDETYKVAITRFDQRIRVGGMAEIAGFDLSLN
PRRRETLEMITTDLYPEGGDISQATFWTGLRPATPDGTPIVGATRYRNLFLNTGHGTLGWTMACG
SGRYLADLMAKKRPQISTEGLDISRYSNSPENAKNAHPAPAH

The role of VIR4 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT5

A *Pseudomonas* bacterial mutant (MUT5) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding imidazoleglycerol-phosphate synthase, cyclase subunit (hisF ; PA5140). This gene encodes the VIR5 nucleic acid (SEQ ID NO:9) shown in Table 7A.

Table 7A. VIR5 Nucleotide Sequence (SEQ ID NO:9)

ATGGCACTGGCAAAACGCATCATCCCCTGCCTCGACGTGGACAACGGCCGAGTGGTCAAGGGCGTCA

```
AGTTCGAGAACATCCGCGACGCCGGCGACCCGGTCGAGATCGCTCGCCGCTACGACGAGCAGGGTGC
CGACGAGATCACCTTCCTCGATATCACCGCCAGCGTCGACGGGCGCGACACCACCCTGCATACCGTC
GAGCGCATGGCTAGCCAGGTGTTCATTCCGCTGACCGTGGGCGGCGGCGTACGCAGCGTGCAGGACA
TCCGCAACCTGTTGAATGCCGGCGCGGACAAGGTCTCGATCAACACCGCCGCGGTGTTCAACCCCGA
GTTCGTCGGTGAGGCCGCCGACCGCTTCGGCTCGCAGTGCATCGTGGTCGCCATCGACGCGAAGAAG
GTTTCCGCCCCGGGCGAGGCGCCGCGCTGGGAAATCTTCACCCATGGCGGGCGCAAGCCCACCGGGC
TGGATGCCGTGCTCTGGGCGAAGAAGATGGAAGACTTGGGCGCTGGCGAGATTCTCCTGACCAGCAT
GGACCAGGACGGCGTGAAGAGCGGTTACGACCTGGGCGTGACCCGCGCCATCAGCGAGGCGGTGAAC
GTGCCGGTGATCGCTTCCGGCGGCGTCGGCAACCTGGAGCACCTGGCCGCCGGCATCCTCGAGGGCA
AGGCCGACGCGGTGCTCGCGGCGAGCATCTTCCACTTCGGCGAGTACACCGTGCCGGAAGCCAAGGC
CTACCTGGCCAGCCGCGGTATCGTGGTGCGCTGA
```

The VIR5 protein (SEQ ID NO:10) encoded by SEQ ID NO:9 is presented using the one-letter amino acid code in Table 7B.

Table 7B. Encoded VIR5 protein sequence (SEQ ID NO:10)

```
MALAKRIIPCLDVDNGRVVKGVKFENIRDAGDPVEIARRYDEQGADEITFLDITASVDGRDTTLH
TVERMASQVFIPLTVGGGVRSVQDIRNLLNAGADKVSINTAAVFNPEFVGEAADRFGSQCIVVAI
DAKKVSAPGEAPRWEIFTHGGRKPTGLDAVLWAKKMEDLGAGEILLTSMDQDGVKSGYDLGVTRA
ISEAVNVPVIASGGVGNLEHLAAGILEGKADAVLAASIFHFGEYTVPEAKAYLASRGIVVR
```

MUT6

A *Pseudomonas* bacterial mutant (MUT6) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding N-acetyl-• –glutamyl-phosphate reductase (ArgC; PA0662). This gene encodes the VIR6 nucleic acid (SEQ ID NO:11) shown in Table 8A.

Table 8A. VIR6 Nucleotide Sequence (SEQ ID NO:11)

```
ATGATCAAGGTCGGCATCGTTGGCGGTACGGGTTATACGGGCGTGGAACTGCTGCGCCTGCTGGCGC
AGCATCCGCAGGCCCGGGTGGAAGTGATCACTTCGCGTTCCGAGGCGGGGGTGAAGGTCGCCGACAT
GTACCCGAACCTGCGAGGTCATTATGACGACCTGCAGTTCAGCGTGCCGGACGCGCAGCGCCTCGGC
GCCTGCGACGTGGTGTTCTTCGCCACGCCGCACGGCGTGGCGCACGCGCTGGCTGGCGAACTGCTGG
ACGCCGGGACCCGGGTCATCGATCTGTCCGCTGACTTCCGCCTGGCGGACGCCGAGGAGTGGGCGCG
CTGGTACGGCCAGCCGCATGGCGCTCCGGCGCTGCTCGACGAGGCTGTCTACGGCCTGCCGGAAGTG
AACCGCGAGAAGATCCGCCAGGCCCGCCTGATCGCCGTGCCGGGCTGCTACCCGACCGCGACCCAGC
TGGGCCTGATCCCGCTGCTGGAAGCCGGCCTGGCCGACGCCTCGCGGCTGATCGCCGATTGCAAGTC
CGGGGTCAGCGGTGCCGGTCGGGGCGCCAAGGTTGGCTCGCTGTTCTGCGAGGCGGGCGAAAGCATG
ATGGCCTACGCGGTCAAAGGGCATCGGCATCTCCCGGAAATCAGCCAGGGCCTGCGTCGGGCCTCCG
GCGGCGACGTCGGGCTGACGTTCGTACCGCACCTGACGCCAATGATCCGCGGTATCCATGCAACCCT
CTATGCCCATGTCGCGGATCGCTCGGTCGACCTCCAGGCGTTGTTCGAGAAGCGCTACGCCGACGAA
CCCTTCGTCGACGTGATGCCGGCCGGCAGCCATCCGGAGACCCGCAGCGTGCGTGGCGCCAATGTCT
GCCGAATCGCCGTGCATCGCCCCCAGGGCGGCGACCTGGTGGTGGTGCTGTCGGTGATCGACAACCT
GGTCAAGGGCGCCTCGGGTCAGGCGCTCCAGAACATGAACATCCTGTTCGGGCTGGACGAGCGCCTG
GGCCTCTCGCATGCGGCCCTGCTCCCCTGA
```

The VIR6 protein (SEQ ID NO:12) encoded by SEQ ID NO:11 is presented using the one-letter amino acid code in Table 8B.

Table 8B. Encoded VIR6 protein sequence (SEQ ID NO:12)

```
MIKVGIVGGTGYTGVELLRLLAQHPQARVEVITSRSEAGVKVADMYPNLRGHYDDLQFSVPDAQR
LGACDVVFFATPHGVAHALAGELLDAGTRVIDLSADFRLADAEEWARWYGQPHGAPALLDEAVYG
LPEVNREKIRQARLIAVPGCYPTATQLGLIPLLEAGLADASRLIADCKSGVSGAGRGAKVGSLFC
EAGESMMAYAVKGHRHLPEISQGLRRASGGDVGLTFVPHLTPMIRGIHATLYAHVADRSVDLQAL
FEKRYADEPFVDVMPAGSHPETRSVRGANVCRIAVHRPQGGDLVVVLSVIDNLVKGASGQALQNM
NILFGLDERLGLSHAALLP
```

The role of VIR6 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT7

A *Pseudomonas* bacterial mutant (MUT7) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding dihydrolipoamide acetyltransferase (AceF; PA5016). This gene encodes the VIR7 nucleic acid (SEQ ID NO:13) is shown in Table 9A.

Table 9A. VIR7 Nucleotide Sequence (SEQ ID NO:13)

```
GTGAGCGAACTCATTCGCGTACCCGACATCGGCAACGGTGAGGGTGAAGTCATCGAGCTGCTGGTCA
AGCCCGGCGACAAGGTCGAGGCCGATCAGAGCCTGCTGACCCTGGAATCCGACAAGGCCAGCATGGA
AATCCCCAGTCCCAAGGCCGGGGTAGTGAAAAGCATCAAGGCGAAGGTCGGCGACACCTTGAAAGAA
GGTGACGAAATCCTCGAGCTGGAAGTGGAAGGCGGCGAACAGCCTGCCGAAGCCAAGGCCGAGGCAG
CGCCCGCCCAACCGGAAGCGCCGAAAGCCGAAGCGCCTGCTCCCGCCCCGAGCGAGAGCAAGCCGGC
CGCCCCCGCCGCGGCCAGCGTCCAGGACATCAAGGTCCCGGACATCGGCTCGGCCGGCAAGGCCAAC
GTCATCGAAGTGATGGTCAAGGCCGGCGACACGGTCGAGGCCGACCAGTCGCTGATCACCCTGGAAT
CCGACAAGGCCAGCATGGAGATCCCCTCGCCGGCCTCCGGGGTGGTGGAAAGCGTCTCGATCAAGGT
CGGTGACGAAGTCGGCACCGGCGACCTGATCCTCAAGCTGAAGGTGGAAGGCGCCGCTCCGGCAGCC
GAAGAGCAACCGGCAGCCGCTCCGGCCCAGGCCGCGGCGCCCGCCGCCGAGCAGAAGCCCGCCGCGG
CGGCCCCTGCGCCAGCCAAGGCCGATACCCCGGCTCCGGTCGGCGCACCCAGCCGCGACGGCGCCAA
GGTCCACGCCGGCCCGGCGGTGCGCATGCTGGCGCGCGAGTTCGGCGTCGAGCTGAGCGAAGTGAAA
GCCAGCGGTCCCAAGGGTCGCATCCTCAAGGAAGACGTCCAGGTCTTCGTCAAGGAGCAACTGCAGC
GCGCCAAGTCCGGCGGTGCCGGCGCCACCGGCGGAGCCGGCATCCCGCCGATCCCGGAAGTCGACTT
CAGCAAGTTCGGCGAAGTGGAAGAAGTGGCGATGACCCGCCTGATGCAGGTCGGCGCCGCCAACCTG
CATCGCAGCTGGCTGAACGTGCCGCACGTGACCCAGTTCGACCAGTCGGACATCACCGACATGGAAG
CCTTCCGCGTTGCCCAGAAGGCCGCGGCGGAGAAGGCCGGGGTCAAGCTGACCGTACTGCCGATCCT
GCTCAAGGCCTGCGCCCACCTGCTCAAGGAACTGCCGGACTTCAACAGTTCGCTGGCCCCCAGCGGC
AAGGCGCTGATCCGCAAGAAGTACGTACACATCGGCTTCGCCGTGGACACTCCGGACGGCCTGCTGG
TCCCGGTGATCCGCGATGTCGACCGGAAGAGCCTCCTGCAACTGGCCGCCGAGGCCGCCGACCTGGC
CGACAAGGCCCGCAACAAGAAGCTCTCGGCCGATGCCATGCAGGGCGCCTGCTTCACCATCTCCAGT
CTCGGCCACATCGGCGGCACCGGCTTCACGCCGATCGTCAACGCGCCGGAAGTGGCGATCCTCGGTG
```

TGTCCAAGGCGACCATGCAGCCGGTATGGGACGGCAAGGCCTTCCAGCCGCGCCTGATGCTGCCGCT
GTCGCTGTCCTACGACCATCGCGTGATCAACGGTGCCGCCGCGGCGCGCTTCACCAAGCGCCTGGGC
GAGCTGCTGGCGGACATCCGCACCCTGCTCCTGTAA

The VIR7 protein (SEQ ID NO:14) encoded by SEQ ID NO:13 is presented using the one-letter amino acid code in Table 9B.

Table 9B. Encoded VIR7 protein sequence (SEQ ID NO:14)

MSELIRVPDIGNGEGEVIELLVKPGDKVEADQSLLTLESDKASMEIPSPKAGVVKSIKAKVGDTL
KEGDEILELEVEGGEQPAEAKAEAAPAQPEAPKAEAPAPAPSESKPAAPAAASVQDIKVPDIGSA
GKANVIEVMVKAGDTVEADQSLITLESDKASMEIPSPASGVVESVSIKVGDEVGTGDLILKLKVE
GAAPAAEEQPAAAPAQAAAPAAEQKPAAAAPAPAKADTPAPVGAPSRDGAKVHAGPAVRMLAREF
GVELSEVKASGPKGRILKEDVQVFVKEQLQRAKSGGAGATGGAGIPPIPEVDFSKFGEVEEVAMT
RLMQVGAANLHRSWLNVPHVTQFDQSDITDMEAFRVAQKAAAEKAGVKLTVLPILLKACAHLLKE
LPDFNSSLAPSGKALIRKKYVHIGFAVDTPDGLLVPVIRDVDRKSLLQLAAEAADLADKARNKKL
SADAMQGACFTISSLGHIGGTGFTPIVNAPEVAILGVSKATMQPVWDGKAFQPRLMLPLSLSYDH
RVINGAAAARFTKRLGELLADIRTLLL

MUT8

A *Pseudomonas* bacterial mutant (MUT8) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding NADH dehydrogenase I chain H (nuoH; PA2643). This gene encodes the VIR8 nucleic acid (SEQ ID NO:15) shown in Table 10A.

Table 10A. VIR8 Nucleotide Sequence (SEQ ID NO:15)

ATGAGTTGGCTGACTCCCGCTCTGGTCACCATCATCCTCACCGTGGTCAAGGCCATCGTGGTGCTGC
TCGCCGTGGTCATCTGCGGCGCCCTGCTAAGCTGGGTCGAGCGCCGCCTGCTCGGCCTCTGGCAGGA
CCGCTACGGCCCCAACCGGGTCGGTCCGTTCGGTGCGTTCCAGCTCGGCGCGGACATGGTCAAGATG
TTCTTCAAGGAGGACTGGACCCCGCCGTTCGCCGACAAGATGATCTTCACCCTGGCCCCGGTAATCG
CGATGGGCGCCCTGCTCGTCGCCTTCGCCATCGTGCCGATCACCCCCACCTGGGGCGTGGCGGACCT
GAACATCGGCATCCTGTTCTTCTTCGCCATGGCCGGCCTGACGGTGTACGCCGTGCTGTTCGCCGGC
TGGTCGAGCAACAACAAGTTCGCCCTGCTCGGCAGCCTGCGCGCCTCGGCCCAGACCATCTCCTACG
AGGTGTTCCTGGCCCTGTCGCTGATGGGCATCGTCGCCCAGGTCGGCTCGTTCAACATGCGCGACAT
CGTCCAGTACCAGATCGACAACGTCTGGTTCATCATTCCGCAGTTCTTCGGCTTCTGCACCTTCATC
ATCGCCGGCGTCGCCGTGACCCACCGTCACCCGTTCGACCAGCCGGAAGCGGAGCAGGAACTGGCGG
ACGGCTACCACATCGAGTACGCCGGGATGAAATGGGGCATGTTCTTCGTCGGCGAGTACATCGGCAT
CGTACTGGTCTCGGCGCTGCTGGCGACCCTGTTCTTCGGCGGCTGGCACGGTCCGTTCCTGGACACC
CTGCCCTGGCTGTCGTTCTTCTACTTCGCCGCCAAGACCGGCTTCTTCATCATGCTCTTCATCCTGA
TCCGCGCCTCGCTGCCGCGTCCGCGCTATGACCAGGTGATGGCGTTCAGCTGGAAGGTGTGCCTGCC
GCTGACCCTGATCAACCTGCTGGTGACCGGCGCGCTCGTGCTGGCCGCGGCCCAGTAA

The VIR8 protein (SEQ ID NO:16) encoded by SEQ ID NO:15 is presented using the one-letter amino acid code in Table 10B.

Table 10B. Encoded VIR8 protein sequence (SEQ ID NO:16)

```
MSWLTPALVTIILTVVKAIVVLLAVVICGALLSWVERRLLGLWQDRYGPNRVGPFGAFQLGADMV
KMFFKEDWTPPFADKMIFTLAPVIAMGALLVAFAIVPITPTWGVADLNIGILFFFAMAGLTVYAV
LFAGWSSNNKFALLGSLRASAQTISYEVFLALSLMGIVAQVGSFNMRDIVQYQIDNVWFIIPQFF
GFCTFIIAGVAVTHRHPFDQPEAEQELADGYHIEYAGMKWGMFFVGEYIGIVLVSALLATLFFGG
WHGPFLDTLPWLSFFYFAAKTGFFIMLFILIRASLPRPRYDQVMAFSWKVCLPLTLINLLVTGAL
VLAAAQ
```

MUT9

A *Pseudomonas* bacterial mutant (MUT9) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyoverdine synthase D (PvdD; PA2399). This gene encodes the VIR9 nucleic acid (SEQ ID NO:17) shown in Table 11A.

Table 11A. VIR9 Nucleotide Sequence (SEQ ID NO:17)

```
GTGCAAGCACTCATAGAGAAGGTGGGCTCCCTTTCCCCCCAGGAAAGGAAGGCATTGGCTGTCCTGC
TCAAGCAGCAAGGTGTCAATCTCTTCGAGATCGCGCCAGTGTTCAAGCGCCAGGACGGCGAGCCCCT
GCGGCTCTCCTATGCCCAGGAGCGACAGTGGTTTCTCTGGCAACTGGAGCCGGAAAGCGCGGCCTAC
CATATCCCGAGTGTCTTGCGTCTACGTGGGCGGCTGGACCTGGATGCCCTGCAACGCAGCTTCGACA
GCCTGGTTGCGCGGCACGAGACCCTACGCACCCGTTTTCGCCTCGACGGCGACGAGGCGCGCCAGGA
GATCGCCGCATCCATGGCATTGCCGTTGGATATCGTCGCGTTGGGGCCGCTCGAGGAGGGCGCCCTC
GCTCGGCAGGTCGAGACGACGATCGCGCGGCCGTTCGACCTGGAGCGTGGGCCGCTGCTGCGGGTGA
GCCTGTTGCGGCTGGCCGAGGACGACCATGTGCTGGTGCTGGTCCAGCATCACATCGTGTCCGACGG
TTGGTCGATGCAGGTGATGGTCGAGGAACTGGTCCAGCTCTATGCCGCCTATAGTCGAGGGCTCGAG
GTAGCGCTGCCGGCTTTGCCGATCCAGTACGCGGACTACGCCCTGTGGCAGCGCAGCTGGATGGAGG
CCGGGGAAAAGGAGCGCCAGTTGGCGTACTGGACCGGCCTGCTGGGCGGCGAGCAGCCGGTGCTGGA
GTTGCCGTTCGACCGGCCGCGCCCGGTTCGGCAAAGCCATCGTGGTGCCCAGTTCATCCTGGAACTG
GATATTGATCTGTCCCAGGCGCTCAGGCGCGTGGCCCAGCAGGAGGGGGCTACTGCCTTCGCCCTGT
TGCTGGCTTCGTTCCAGGCGCTGCTGTATCGCTACAGCGGGCAGGCGGATATCCGTGTCGGCGTGCC
GATCGCCAATCGCAACCGCGTGGAGACCGAGCGGCTGATCGGCTTCTTCGTCAACACCCAGGTGCTC
AAGGCCGACCTGGACGGTCGGATGGGCTTCGACGAGCTGCTGGCCCAGGCCCGCCAACGCGCGCTGG
AGGCCCAGGCGCACCAGGACCTGCCGTTCGAGCAACTGGTGGAGGCCTTGCAGCCGGAGCGCAGTCT
TAGCCACAACCCGCTGTTCCAGGTGCTGTTCAACTACCAGAGCGAAGCCCGTGGCAACGGCCAGGCA
TTCCGCTTCGACGAGTTACAGATGGAAAGCGTGCAGTTCGACAGCCGGACGGCGCAGTTCGACTTGA
CGTTGGACCTGACGGACGAAGAGCAGCGTTTTTGCGCCGTTTTCGACTACGCCACCGACCTGTTCGA
CGCCTCCACCGTGGAACGCCTGGCCGGCCATTGGCGCAACCTGTTGCGCGGCATCGTCGCCAACCCA
CGACAGCGGCTCGGCGAGTTGCCGCTGCTGGATGCGCCGGAGCGCCGGCAGACCCTCTCCGAATGGA
ACCCGGCCCAGCGCGAGTGCGCGGTGCAGGGCACCTTGCAGCAGCGTTTCGAGGAACAGGCGCGGCA
ACGGCCACAGGCGGTTGCGCTGATCCTCGACGAACAACGGTTGAGCTACGGCGAACTGAATGCGCGG
GCCAATCGCCTGGCGCACTGCCTGATCGCCCGTGGCGTTGGCGCGGACGTGCCGGTCGGGCTGGCGC
TGGAGCGTTCGCTGGACATGCTGGTCGGCTTGCTGGCGATCCTCAAGGCCGGCGGCGCCTACCTGCC
GTTGGACCCGGCGGCGCCAGAGGAGCGCCTGGCGCATATCCTCGACGACAGTGGGGTACGGCTGCTG
CTGACCCAGGGGCATCTGCTCGAGCGCCTGCCACGGCAGGCGGGGGTGGAGGTGCTGGCCATCGACG
GACTGGTGCTGGACGGCTACGCCGAGAGCGATCCGCTCCCGACGCTATCGGCGGACAACCTGGCCTA
```

CGTGATCTATACCTCGGGCTCGACCGGCAAGCCCAAGGGCACATTGCTCACCCACCGCAACGCGCTG
CGCCTGTTCAGCGCCACCGAGGCCTGGTTCGGCTTCGACGAGCGGGACGTGTGGACATTGTTCCATT
CCTACGCCTTCGATTTCTCGGTCTGGGAAATCTTCGGCGCGCTGCTCTATGGCGGGTGCCTGGTGAT
TGTGCCGCAATGGGTGAGCCGTTCGCCGGAAGACTTCTACCGTCTGCTGTGCCGCGAAGGCGTGACG
GTGCTCAACCAGACGCCGTCGGCGTTCAAGCAACTGATGGCGGTGGCCTGTTCCGCCGACATGGCGA
CGCAGCAGCCGGCGCTGCGCTACGTGATCTTCGGTGGCGAGGCGCTGGATCTGCAGAGCCTGCGGCC
GTGGTTCCAGCGCTTCGGCGATCGCCAGCCGCAACTGGTGAACATGTACGGCATCACCGAGACCACG
GTGCACGTAACCTACCGTCCGGTGAGCGAGGCCGACCTGGAAGGTGGCCTGGTCAGTCCGATTGGCG
GGACCATCCCGGACCTGTCCTGGTACATCCTCGACCGTGACCTGAACCCGGTGCCGCGCGGCGCGGT
GGGCGAGCTGTACATCGGTCGCGCCGGGCTGGCGCGCGGCTACCTGAGGCGGCCCGGGTTGAGTGCC
ACCCGCTTCGTGCCGAACCCGTTCCCCGGCGGCGCCGGCGAGCGGCTGTACCGTACCGGCGACCTGG
CACGGTTCCAGGCGGATGGCAATATCGAGTACATCGGGCGTATCGACCACCAGGTGAAGGTTCGCGG
CTTCCGTATCGAACTGGGCGAGATCGAAGCGGCGCTCGCCGGTCTGGCCGGGGTACGCGATGCCGTG
GTGCTGGCCCATGACGGAGTCGGCGGCACGCAACTGGTGGGATACGTGGTGGCGGACTCGGCGGAGG
ATGCCGAGCGTCTGCGGGAGTCGCTGCGGGAGTCGCTGAAGCGGCACCTGCCGGACTACATGGTGCC
GGCGCACCTGATGCTGCTGGAGCGGATGCCGCTGACGGTCAATGGCAAGCTCGACCGGCAGGCGTTG
CCGCAACCGGATGCGAGCCTGTCGCAACAGGCCTATCGAGCGCCCGGTAGCGAGCTGGAGCAGCGCA
TCGCAGCGATCTGGTCGGAGATCCTGGGAGTGGAACGGGTCGGCCTGGACGACAACTTCTTCGAACT
GGGCGGTCATTCGTTGCTGGCTACCCGGGTGATTTCTCGGGTTCGCCAGGAGCAGCAGTTGGACGCA
AGCCTGAAGGCGTTGTTCGAGCGGCCGGTTCTGGAAGCGTTCGCCCAGGGATTGGAACGCACGACGG
ATGCGGTCTCGACGATACCGCTTGCCGATCGGCAGCAACCGTTGGCACTGTCCTTCGCTCAGGAGCG
TCAGTGGTTCCTCTGGCAACTGGAGCCGGAAAGCGCGGCCTACCATATTCCGAGTGCCTTGCGCCTA
CGCGGGCGGCTGGACGTGGATGCCTTGCAACGCAGCTTCGACAGCCTGGTCGCGCGGCATGAAACCT
TGCGTACCCGCTTCCGGCTGGAGGGAGGGCGTTCGTACCAGCAGGTACAACCTGCGGTTAGCGTTTC
CATCGAGCGGGAACAGTTCGGTGAAGAAGGCCTGATCGAACGGATACAGGCCATCGTTGTGCAGCCA
TTCGACCTGGAACGGGGGCCGCTGCTGCGGGTGAACCTGTTGCAACTGGCCGAGGACGACCATGTAC
TGGTGCTGGTCCAGCACCACATCGTGTCCGATGGTTGGTCGATGCAGGTGATGGTCGAGGAACTGGT
CCAGCTCTATGCCGCCTATAGCCAAGGGCTCGACGTGGTGTTGCCAGCCCTGCCGATCCAGTACGCG
GACTACGCCCTGTGGCAGCGCAGCTGGATGGAGGCGGGGGAAAAGGAGCGCCAGTTGGCGTACTGGA
CCGGCCTGCTGGGCGGCGAGCAGCCGGTGCTGGAGTTGCCGTTCGATCGGCCGCGTCCGGCCCGGCA
GAGCCATCGTGGCGCGCAGTTGGGTTTCGAGCTATCGCGGGAACTGGTCGAGGCCGTGAGAGCCTTG
GCCCAGCGTGAAGGCGCCAGTAGTTTCATGCTGTTGCTGGCCTCGTTCCAGGCGCTGTTGTATCGCT
ACAGCGGGCAGGCGGATATCCGTGTCGGTGTGCCGATCGCCAATCGCAACCGCGTGGAGACCGAGCG
GCTGATCGGCTTCTTCGTCAACACCCAGGTGCTCAAGGCCGACCTGGACGGTCGGATGGGCTTCGAC
GAGCTGCTGGCCCAGGCCCGCCAACGCGCGCTGGAGGCCCAGGCGCACCAGGACCTGCCGTTCGAGC
AACTGGTGGAAGCCTTGCAGCCGGAGCGCAATGCCAGCCACAACCCACTGTTCCAGGTGCTGTTCAA
CCATCAGAGCGAGATACGCTCGGTGACGCCCGAGGTTCAGTTGGAGGACCTGCGTCTGGAAGGCCTG
GCCTGGGACGGCCAGACTGCGCAGTTCGACCTGACGCTGGATATTCAGGAAGACGAAAACGGCATCT
GGGCCTCCTTCGACTATGCCACCGATCTGTTCGACGCCTCCACCGTGGAACGCCTGGCCGGCCATTG
GCGCAACCTGTTGCGCGGCATCGTCGCCAACCCACGACAGCGGCTCGGCGAGTTGCCGCTGCTGGAT
GCGCCGGAGCGCCGGCAGACCCTCTCCGAATGGAACCCGGCCCAGCGCGAGTGCGCGGTGCAGGGCA
CCTTGCAGCAGCGTTTCGAGGAGCAGGCGCGGCAACGGCCACAGGCGGTTGCGCTGATCCTCGACGA
ACAACGGTTGAGCTACGGCGAACTGAATGCGCGGGCCAATCGCCTGGCGCACTGCCTGATCGCTCGC
GGCGTTGGCGCGGACGTGCCGGTCGGGCTGGCGCTGGAGCGTTCGCTGGACATGCTGGTCGGCTTGC
TGGCGATCCTCAAGGCCGGCGGCGCCTACCTGCCGTTGGACCCGGCGGCGCCAGAGGAGCGCCTGGC
GCATATCCTCGACGACAGTGGGGTACGGCTGCTGCTGACCCAGGGGCATCTGCTCGAGCGCCTGCCG
CGGCAGGCGGGGGTGGAGGTGCTGGCCATCGACGGACTGGTGCTGGACGGCTACGCCGAGAGCGATC
CGCTCCCGACGCTATCGGCGGACAACCTGGCCTACGTGATCTATACCTCGGGCTCGACCGGCAAGCC
CAAGGGCACGTTGCTCACCCACCGCAACGCGCTGCGCCTGTTCAGCGCCACCGAGGCCTGGTTCGGC
TTCGACGAGCGGGACGTGTGGACGTTGTTCCATTCCTACGCCTTCGATTTCTCGGTCTGGGAAATCT
TCGGCGCGCTGCTCTATGGCGGGCGCCTGGTGATCGTGCCGCAATGGGTGAGCCGTTCGCCGGAAGA
CTTCTACCGTCTGCTGTGCCGCGAAGGCGTGACGGTGCTCAACCAGACGCCGTCGGCGTTCAAGCAA
CTGATGGCGGTGGCCTGTTCCGCCGACATGGCGACGCAGCAGCCGGCGCTGCGCTACGTGATCTTCG
GTGGCGAGGCGCTGGATCTGCAGAGCCTGCGGCCGTGGTTCCAGCGCTTTGGCGATCGCCAGCCGCA
ACTGGTGAACATGTACGGCATCACCGAGACCACGGTACACGTAACCTACCGTCCGGTGAGCGAAGCC
GACCTGAAGGGTGGCCTGGTCAGTCCGATCGGCGGGACCATCCCGGACCTGTCCTGGTACATCCTCG
ACCGTGACCTGAACCCGGTGCCGCGCGGCGGTGGGCGAGCTGTACATCGGTCGCGCCGGTCTGGC
GCGCGGCTACCTGAGGCGGCCCGGGTTGAGTGCCACCCGCTTCGTGCCGAACCCGTTCCCCGGCGGT
GCCGGCGAGCGGCTGTACCGTACCGGCGACCTGGCACGGTTCCAGGCGGATGGCAATATCGAGTACA
TCGGGCGTATCGACCACCAGGTGAAGGTTCGCGGCTTCCGTATCGAACTGGGTGAGATCGAAGCGGC
GCTCGCCGGTCTGGCCGGGGTACGCGATGCCGTGGTGCTGGCCCATGACGGGGTCGGCGGCACGCAA
CTGGTGGGATACGTGGTGGCGGACTCGGCGGAGGATGCCGAGCGTCTGCGGGAGTCGCTGCGGGAGT
CGCTGAAGCGGCACCTGCCGGACTACATGGTGCCGGCGCACCTGATGCTGCTGGAGCGGATGCCGCT
GACGGTCAATGGCAAGCTCGACCGGCAGGCGTTGCCGCAACCGGATGCGAGCTTGTCGCAGCAGGCC
TATCGAGCGCCCGGTAGCGAGCTGGAGCAGCGCATCGCAGCGATCTGGGCGGAGATCCTGGGAGTGG

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AACGGGTCGGCCTGGACGACAACTTCTTCGAACTGGGCGGTCACTCATTGTTGCTGCTGATGCTCAA
GGAGCGGATCGGCGATACCTGCCAGGCTACGCTGAGCATCAGCCAACTGATGACCCATGCCAGCGTC
GCGGAACAGGCGGCATGCATCGAGGGGCAGGCGCGTGAGTCGTTGCTGGTGCCGCTCAACGGCAGGC
GCGAAGGTTCGCCGCTGTTCATGTTCCATCCGAGTTTCGGCTCTGTGCACTGTTACAAGACCCTCGC
CATGGCGCTGCGGGATCGTCATCCGGTCAAGGGTGTTGTCTGCCGTGCCCTGCTGGGCGCTGGTCGC
GAGGTGCCGGAGTGGGACGATATGGTTGCGGAATACGCCGAGCAATTGCTGCAGGAGCACCCCGAAG
GGGTTTTCAACCTGGCGGGATGGTCGCTCGGCGGCAACCTGGCGATGGATGTCGCGGCCCGGCTGGA
GCAGCGTGGGCGGCAGGTGGCTTTCGTCGGCTGGATCGATGCACCGGCACCGGTCAGGGTCGAAGCG
TTCTGGAACGAGATCGGGCCGACGCCGGAGGCAGTCCCGAACCTATCCGTGGGCGAGATGCGGGTGG
AACTGCTCGGTGTCATGTTTCCGGAGCGGGCCGAGCATATCGAACGGGCCTGGTCATCGATCTGCTC
CGCCACGACGGACGATGAGCAGCGCTGGACGAGGATGAGCGACTGGGCGGAAGCGGAGATCGGCGCC
GAGTTCGCGACACTGCGCAGCGAAATCGCACAGAGCAACGAACTGGAAGTGTCCTGGGAGTTGAAAC
AGATCCTCGACGAGCGCCTGAAAGCGATGGATTACCCGCGTCTGACGGCGAAGGTCAGCCTCTGGTG
GGCCGCGCGCAGCACCAATGCCATCCAGCGGAGCGCGGTGGAGCGCTCGATGGCCGAGGCGATCGGG
GCTGAGCGTGTCGAACCGGTGCGGGTGCTGGATACCCGGCACGACAAGATCATCGACCACCCTGAGT
TTGTGCAGAGCTTCCGGGCCGCCCTGGAGCGTGCCGGGCGCTGA
```

The VIR9 protein (SEQ ID NO:18) encoded by SEQ ID NO:17 is presented using the one-letter amino acid code in Table 11B.

Table 11B. Encoded VIR9 protein sequence (SEQ ID NO:18)

```
MQALIEKVGSLSPQERKALAVLLKQQGVNLFEIAPVFKRQDGEPLRLSYAQERQWFLWQLEPESA
AYHIPSVLRLRGRLDLDALQRSFDSLVARHETLRTRFRLDGDEARQEIAASMALPLDIVALGPLE
EGALARQVETTIARPFDLERGPLLRVSLLRLAEDDHVLVLVQHHIVSDGWSMQVMVEELVQLYAA
YSRGLEVALPALPIQYADYALWQRSWMEAGEKERQLAYWTGLLGGEQPVLELPFDRPRPVRQSHR
GAQFILELDIDLSQALRRVAQQEGATAFALLLASFQALLYRYSGQADIRVGVPIANRNRVETERL
IGFFVNTQVLKADLDGRMGFDELLAQARQRALEAQAHQDLPFEQLVEALQPERSLSHNPLFQVLF
NYQSEARGNGQAFRFDELQMESVQFDSRTAQFDLTLDLTDEEQRFCAVFDYATDLFDASTVERLA
GHWRNLLRGIVANPRQRLGELPLLDAPERRQTLSEWNPAQRECAVQGTLQQRFEEQARQRPQAVA
LILDEQRLSYGELNARANRLAHCLIARGVGADVPVGLALERSLDMLVGLLAILKAGGAYLPLDPA
APEERLAHILDDSGVRLLLTQGHLLERLPRQAGVEVLAIDGLVLDGYAESDPLPTLSADNLAYVI
YTSGSTGKPKGTLLTHRNALRLFSATEAWFGFDERDVWTLFHSYAFDFSVWEIFGALLYGGCLVI
VPQWVSRSPEDFYRLLCREGVTVLNQTPSAFKQLMAVACSADMATQQPALRYVIFGGEALDLQSL
RPWFQRFGDRQPQLVNMYGITETTVHVTYRPVSEADLEGGLVSPIGGTIPDLSWYILDRDLNPVP
RGAVGELYIGRAGLARGYLRRPGLSATRFVPNPFPGGAGERLYRTGDLARFQADGNIEYIGRIDH
QVKVRGFRIELGEIEAALAGLAGVRDAVVLAHDGVGGTQLVGYVVADSAEDAERLRESLRESLKR
HLPDYMVPAHLMLLERMPLTVNGKLDRQALPQPDASLSQQAYRAPGSELEQRIAAIWSEILGVER
VGLDDNFFELGGHSLLATRVISRVRQEQQLDASLKALFERPVLEAFAQGLERTTDAVSTIPLADR
QQPLALSFAQERQWFLWQLEPESAAYHIPSALRLRGRLDVDALQRSFDSLVARHETLRTRFRLEG
GRSYQQVQPAVSVSIEREQFGEEGLIERIQAIVVQPFDLERGPLLRVNLLQLAEDDHVLVLVQHH
IVSDGWSMQVMVEELVQLYAAYSQGLDVVLPALPIQYADYALWQRSWMEAGEKERQLAYWTGLLG
GEQPVLELPFDRPRPARQSHRGAQLGFELSRELVEAVRALAQREGASSFMLLLASFQALLYRYSG
QADIRVGVPIANRNRVETERLIGFFVNTQVLKADLDGRMGFDELLAQARQRALEAQAHQDLPFEQ
LVEALQPERNASHNPLFQVLFNHQSEIRSVTPEVQLEDLRLEGLAWDGQTAQFDLTLDIQEDENG
IWASFDYATDLFDASTVERLAGHWRNLLRGIVANPRQRLGELPLLDAPERRQTLSEWNPAQRECA
VQGTLQQRFEEQARQRPQAVALILDEQRLSYGELNARANRLAHCLIARGVGADVPVGLALERSLD
MLVGLLAILKAGGAYLPLDPAAPEERLAHILDDSGVRLLLTQGHLLERLPRQAGVEVLAIDGLVL
DGYAESDPLPTLSADNLAYVIYTSGSTGKPKGTLLTHRNALRLFSATEAWFGFDERDVWTLFHSY
AFDFSVWEIFGALLYGGRLVIVPQWVSRSPEDFYRLLCREGVTVLNQTPSAFKQLMAVACSADMA
TQQPALRYVIFGGEALDLQSLRPWFQRFGDRQPQLVNMYGITETTVHVTYRPVSEADLKGGLVSP
IGGTIPDLSWYILDRDLNPVPRGAVGELYIGRAGLARGYLRRPGLSATRFVPNPFPGGAGERLYR
TGDLARFQADGNIEYIGRIDHQVKVRGFRIELGEIEAALAGLAGVRDAVVLAHDGVGGTQLVGYV
VADSAEDAERLRESLRESLKRHLPDYMVPAHLMLLERMPLTVNGKLDRQALPQPDASLSQQAYRA
PGSELEQRIAAIWAEILGVERVGLDDNFFELGGHSLLLLMLKERIGDTCQATLSISQLMTHASVA
EQAACIEGQARESLLVPLNGRREGSPLFMFHPSFGSVHCYKTLAMALRDRHPVKGVVCRALLGAG
REVPEWDDMVAEYAEQLLQEHPEGVFNLAGWSLGGNLAMDVAARLEQRGRQVAFVGWIDAPAPVR
VEAFWNEIGPTPEAVPNLSVGEMRVELLGVMFPERAEHIERAWSSICSATTDDEQRWTRMSDWAE
AEIGAEFATLRSEIAQSNELEVSWELKQILDERLKAMDYPRLTAKVSLWWAARSTNAIQRSAVER
SMAEAIGAERVEPVRVLDTRHDKIIDHPEFVQSFRAALERAGR
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MUT10

A *Pseudomonas* bacterial mutant (MUT10) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the RND multidrug efflux transporter MexD (mexD; PA4598). This gene encodes the VIR10 nucleic acid (SEQ ID NO:19) shown in Table 12A.

Table 12A. VIR10 Nucleotide Sequence (SEQ ID NO:19)

ATGTCCGAATTCTTCATCAAGCGGCCGAACTTCGCCTGGGTGGTGGCCCTGTTCATCTCCCTGGCCG
GCCTGCTGGTCATTTCCAAATTGCCGGTAGCGCAGTACCCCAATGTCGCGCCGCCACAGATCACCAT
CACCGCCACCTATCCCGGCGCCTCGGCGAAGGTGCTGGTGGACTCCGTCACCAGTGTGCTCGAGGAG
TCGCTGAACGGCGCCAAGGGCCTGCTCTACTTCGAGTCGACCAACAACTCCAACGGCACCGCCGAGA
TCGTCGTCACCTTCGAGCCGGGCACCGATCCGGACCTGGCCCAGGTGGACGTGCAGAACCGCCTGAA
GAAAGCCGAGGCGCGCATGCCGCAGGCGGTGCTGACCCAGGGCCTGCAGGTCGAGCAGACCAGCGCC
GGTTTCCTGCTGATCTATGCGCTCAGCTACAAGGAAGGCGCTCAGCGCAGCGACACCACCGCCCTCG
GCGACTACGCCGCGCGCAATATCAACAACGAGCTGCGGCGCCTGCCGGGCGTCGGCAAGCTGCAATT
CTTCTCTTCCGAGGCGGCCATGCGGGTCTGGATCGATCCGCAGAAGCTGGTGGGCTTCGGCCTCTCC
ATCGACGACGTGAGCAATGCCATCCGCGGGCAGAACGTGCAGGTGCCGGCCGGCGCCTTCGGCAGCG
CACCGGGCAGTTCCGCGCAGGAGCTGACGGCGACCCTGGCGGTGAAGGGCACCCTGGACGATCCGCA
GGAGTTCGGCCAGGTAGTGCTGCGCGCCAACGAGGACGGCTCGCTGGTCCGGCTCGCCGATGTCGCG
CGCCTGGAACTCGGCAAGGAGAGCTACAACATTTCCTCGCGACTGAACGGCACGCCCACCGTGGGCG
GGGCTATCCAGCTGTCGCCCGGGGCCAACGCGATCCAGACCGCTACCCTGGTGAAACAGCGTCTCGC
CGAACTGTCGGCGTTCTTCCCCGAGGACATGCAGTACAGCGTGCCCTACGACACCTCGCGCTTCGTC
GACGTGGCCATCGAGAAGGTGATCCACACCCTGATCGAAGCGATGGTCCTGGTGTTCCTGGTGATGT
TCCTGTTCCTGCAGAACGTCCGCTACACCCTGATCCCGTCCATCGTGGTGCCGGTGTGCCTGCTGGG
TACGCTGATGGTGATGTACCTGCTGGGGTTCTCGGTGAACATGATGACCATGTTCGGCATGGTCCTG
GCGATCGGCATCCTGGTGGACGACGCCATCGTGGTGGTGGAGAACGTCGAGCGGATCATGGCGGAGG
AGGGGATTTCCCCGGCCGAGGCCACGGTCAAGGCGATGAAGCAGGTATCCGGCGCCATCGTCGGCAT
CACCCTGGTGCTCTCGGCGGTGTTCCTGCCGCTGGCTTTCATGGCCGGTTCGGTGGGGGTGATCTAC
CAGCAGTTCTCGGTGTCGCTGGCGGTCTCGATCCTGTTCTCCGGCTTCCTCGCCCTGACCTTCACCC
CGGCGCTGTGCGCCACGCTGCTCAAGCCCATTCCCGAAGGGCACCACGAGAAGCGCGGCTTCTTCGG
CGCCTTCAACCGTGGCTTCGCCCGCGTCACCGAGCGCTATTCGCTGCTCAACTCGAAGCTGGTGGCG
CGCGCCGGACGCTTCATGCTGGTGTACGCCGGCCTGGTGGCCATGCTCGGCTACTTCTACCTGCGCC
TGCCGGAAGCCTTCGTGCCGGCGGAAGACCTCGGCTACATGGTGGTCGACGTGCAACTGCCGCCTGG
CGCTTCGCGCGTGCGCACCGATGCCACCGGCGAGGAGCTCGAGCGCTTCCTCAAGTCCCGCGAGGCG
GTGGCTTCGGTGTTCCTGATCTCGGGCTTCAGCTTCTCCGGCCAGGGCGACAATGCCGCGCTGGCCT
TCCCAACCTTCAAGGACTGGTCCGAGCGAGGCGCCGAGCAGTCGGCCGCCGCCGAGATCGCCGCGCT
GAACGAGCATTTCGCGCTGCCCGACGATGGCACGGTCATGGCCGTGTCGCCGCCACCGATCAACGGT
CTGGGTAACTCCGGCGGCTTCGCATTGCGCCTGATGGACCGTAGCGGGGTCGGCCGCGAAGCGCTGC
TGCAGGCTCGCGATACTCTTCTTGGCGAGATCCAGACCAACCCGAAATTCCTTTACGCGATGATGGA
AGGACTGGCCGAAGCGCCGCAACTGCGCCTGTTGATCGACCGGGAGAAGGCCCGTGCCCTGGGGGTG
AGCTTCGAGACCATCAGCGGCACGCTGTCCGCTGCCTTCGGCTCGGAGGTGATCAACGACTTCACCA
ATGCGGGGCGCCAACAGCGGGTGGTGATCCAGGCCGAACAGGGCAACCGGATGACCCCGGAAAGCGT
GCTCGAGCTATACGTGCCTAACGCTGCTGGCAACCTGGTACCGCTCAGCGCCTTCGTCAGCGTGAAA
TGGGAAGAGGGACCGGTGCAATTGGTGCGCTATAACGGCTACCCGTCGATCCGCATCGTCGGTGACG
CCGCGCCCGGCTTCAGTACCGGCGAAGCCATGGCGGAAATGGAGCGCCTGGCCTCGCAGCTGCCGGC
CGGCATCGGCTACGAGTGGACCGGCCTGTCCTATCAGGAGAAGGTCTCCGCCGGGCAGGCCACCAGC
CTGTTCGCCCTCGCCATCCTGGTGGTGTTCCTGTTGCTGGTGGCGCTCTACGAGAGCTGGTCGATCC
CGCTGTCGGTGATGCTGATCGTGCCGATCGGCGCCATCGGCGCGGTGCTCGCGGTGATGGTCAGCGG
TATGTCCAACGACGTGTATTTCAAGGTCGGCCTGATCACCATCATCGGTCTTTCGGCGAAGAACGCG
ATCCTCATCGTCGAGTTCGCCAAGGAACTCTGGGAGCAGGGGCATAGCCTGCGCGACGCCGCCATCG
AGGCCGCGCGCCTGCGCTTCCGGCCGATCATCATGACTTCCATGGCGTTCATCCTCGGCGTGATACC
CCTGGCCCTGGCCAGCGGTGCCGGCGCGGCGAGCCAGCGTGCCATCGGCACCGGAGTGATCGGCGGG
ATGCTCAGCGCCACCTTCCTCGGCGTGCTGTTCGTACCTATCTGTTTCGTCTGGCTGCTGTCGCTGC

TGCGCAGCAAGCCGGCACCCATCGAACAGGCCGCTTCGGCCGGGGAGTGA

The VIR10 protein (SEQ ID NO:20) encoded by SEQ ID NO:19 is presented using the one-letter amino acid code in Table 12B.

Table 12B. Encoded VIR10 protein sequence (SEQ ID NO:20)

MSEFFIKRPNFAWVVALFISLAGLLVISKLPVAQYPNVAPPQITITATYPGASAKVLVDSVTSVL
EESLNGAKGLLYFESTNNSNGTAEIVVTFEPGTDPDLAQVDVQNRLKKAEARMPQAVLTQGLQVE
QTSAGFLLIYALSYKEGAQRSDTTALGDYAARNINNELRRLPGVGKLQFFSSEAAMRVWIDPQKL
VGFGLSIDDVSNAIRGQNVQVPAGAFGSAPGSSAQELTATLAVKGTLDDPQEFGQVVLRANEDGS
LVRLADVARLELGKESYNISSRLNGTPTVGGAIQLSPGANAIQTATLVKQRLAELSAFFPEDMQY
SVPYDTSRFVDVAIEKVIHTLIEAMVLVFLVMFLFLQNVRYTLIPSIVVPVCLLGTLMVMYLLGF
SVNMMTMFGMVLAIGILVDDAIVVVENVERIMAEEGISPAEATVKAMKQVSGAIVGITLVLSAVF
LPLAFMAGSVGVIYQQFSVSLAVSILFSGFLALTFTPALCATLLKPIPEGHHEKRGFFGAFNRGF
ARVTERYSLLNSKLVARAGRFMLVYAGLVAMLGYFYLRLPEAFVPAEDLGYMVVDVQLPPGASRV
RTDATGEELERFLKSREAVASVFLISGFSFSGQGDNAALAFPTFKDWSERGAEQSAAAEIAALNE
HFALPDDGTVMAVSPPPINGLGNSGGFALRLMDRSGVGREALLQARDTLLGEIQTNPKFLYAMME
GLAEAPQLRLLIDREKARALGVSFETISGTLSAAFGSEVINDFTNAGRQQRVVIQAEQGNRMTPE
SVLELYVPNAAGNLVPLSAFVSVKWEEGPVQLVRYNGYPSIRIVGDAAPGFSTGEAMAEMERLAS
QLPAGIGYEWTGLSYQEKVSAGQATSLFALAILVVFLLLVALYESWSIPLSVMLIVPIGAIGAVL
AVMVSGMSNDVYFKVGLITIIGLSAKNAILIVEFAKELWEQGHSLRDAAIEAARLRFRPIIMTSM
AFILGVIPLALASGAGAASQRAIGTGVIGGMLSATFLGVLFVPICFVWLLSLLRSKPAPIEQAAS
AGE

MUT11

A *Pseudomonas* bacterial mutant (MUT11) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA3721. This gene encodes the VIR11 nucleic acid (SEQ ID NO:21) shown in Table 13A.

Table 13A. VIR11 Nucleotide Sequence (SEQ ID NO:21)

ATGAACGATGCTTCTCCCCGTCTGACCGAACGCGGCAGGCAACGCCGCCGCGCCATGCTCGACGCCG
CTACCCAGGCCTTTCTCGAACACGGTTTCGAAGGCACCACCCTGGACATGGTGATAGAACGGGCCGG
TGGTTCACGGGGGACCCTGTACAGCTCCTTCGGCGGCAAGGAGGGCCTGTTCGCCGCGGTGATCGCC
CACATGATCGGGGAAATCTTCGACGACAGCGCCGATCAGCCGCGCCCCGCCGCCACGCTGAGCGCCA
CCCTCGAGCATTTCGGCCGGCGCTTTCTCACCAGCCTGCTCGATCCCCGCTGCCAGAGCCTCTATCG
CCTGGTGGTGGCGGAATCCCCGCGGTTTCCGGCGATCGGCAAGTCCTTCTACGAGCAGGGGCCGCAG
CAGAGCTATCTGCTGCTCAGCGAGCGACTGGCCGCGGTCGCTCCTCACATGGACGAGGAAACGCTCT
ACGCGGTGGCCTGCCAGTTTCTCGAGATGCTCAAGGCCGACCTGTTCCTCAAGGCCCTCAGCGTGGC
CGACTTCCAGCCGACCATGGCGCTGCTGGAAACCCGCCTCAAGCTGTCGGTGGACATCATCGCCTGC
TACCTGGAACACCTGTCGCAGAGCCCCGCGCAGGGCTGA

The VIR11 protein (SEQ ID NO:22) encoded by SEQ ID NO:21 is presented using the one-letter amino acid code in Table 13B.

Table 13B. Encoded VIR11 protein sequence (SEQ ID NO:22)

```
MNDASPRLTERGRQRRRAMLDAATQAFLEHGFEGTTLDMVIERAGGSRGTLYSSFGGKEGLFAAV
IAHMIGEIFDDSADQPRPAATLSATLEHFGRRFLTSLLDPRCQSLYRLVVAESPRFPAIGKSFYE
QGPQQSYLLLSERLAAVAPHMDEETLYAVACQFLEMLKADLFLKALSVADFQPTMALLETRLKLS
VDIIACYLEHLSQSPAQG
```

MUT12

A *Pseudomonas* bacterial mutant (MUT12) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA0596. This gene encodes the VIR12 nucleic acid (SEQ ID NO:23) shown in Table 14A.

Table 14A. VIR12 Nucleotide Sequence (SEQ ID NO:23)

```
ATGTCTGATGATGCCCGTTTCCAGCAGCTGAATTGCTGGTTGGACTCTTGTTTGCCCGAGTTGTTCG
TTGCCGAAGGTTGGGGGGAAGTGCCCCCCGCCGAACTGATCCCGGCCAGTAGCGACGCCAGCTTCCG
TCGTTATTTCCGCTGGCAGGGAGGGGACCGCAGCCTGGTGGTGATGGACGCGCCGCCGCCCCAGGAA
GACTGCCGACCGTTCGTCAAGGTCGCCGGACTGCTCGCCGGAGCCGGCGTGCATGTGCCGAGGATTC
TCGCCCAGGACCTGGAGAACGGTTTCCTGCTGCTCAGTGACCTGGGCCGGCAGACCTACCTCGACGT
GCTTCATCCCGGGAATGCCGACGAGCTGTTCGAACCGGCCCTGGATGCGCTGATCGCCTTCCAGAAG
GTCGATGTCGCCGGTGTCCTGCCTGCCTACGACGAAGCGGTGCTGCGCCGCGAGCTGCAGCTGTTCC
CCGACTGGTACCTGGCCCGCCACCTCGGCGTGGAGCTGGAGGGCGAGACGCTGGCCCGCTGGAAACG
GATCTGCGACCTGCTGGTACGCAGCGCGCTGGAGCAACCGCGGGTGTTCGTCCATCGCGACTATATG
CCGCGCAATCTGATGCTCAGCGAGCCCAACCCGGGCGTCCTCGACTTCCAGGACGCCCTGCACGGCC
CGGTCACCTACGATGTCACCTGCCTGTACAAGGACGCCTTCGTCAGTTGGCCGGAGCCGCGCGTGCA
TGCCGCGCTGAACCGTTACTGGAAGAAGGCGACCTGGGCCGGCATCCCGCTGCCGCCAAGCTTCGAA
GACTTCCTCCGTGCCAGCGACCTGATGGGCGTGCAGCGCCACCTGAAGGTGATTGGCATCTTCGCCC
GTATCTGTCACCGCGACGGCAAGCCGCGCTACCTGGGTGACGTGCCGCGCTTCTTCCGTTATCTGGA
AACCGCCGTGGCGCGCCGTCCCGAGCTGGCCGAACTGGGCGAGCTGCTGGCCTCGCTGCCGCAGGGA
GCCGAGGCATGA
```

The VIR12 protein (SEQ ID NO:24) encoded by SEQ ID NO:23 is presented using the one-letter amino acid code in Table 14B.

Table 14B. Encoded VIR12 protein sequence (SEQ ID NO:24)

```
MSDDARFQQLNCWLDSCLPELFVAEGWGEVPPAELIPASSDASFRRYFRWQGGDRSLVVMDAPPP
QEDCRPFVKVAGLLAGAGVHVPRILAQDLENGFLLLSDLGRQTYLDVLHPGNADELFEPALDALI
AFQKVDVAGVLPAYDEAVLRRELQLFPDWYLARHLGVELEGETLARWKRICDLLVRSALEQPRVF
VHRDYMPRNLMLSEPNPGVLDFQDALHGPVTYDVTCLYKDAFVSWPEPRVHAALNRYWKKATWAG
```

IPLPPSFEDFLRASDLMGVQRHLKVIGIFARICHRDGKPRYLGDVPRFFRYLETAVARRPELAEL
GELLASLPQGAEA

MUT13

A *Pseudomonas* bacterial mutant (MUT13) was made by transposon insertion in *a P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA5265. This gene encodes the VIR13 nucleic acid (SEQ ID NO:25) shown in Table 15A.

Table 15A. VIR13 Nucleotide Sequence (SEQ ID NO:25)

ATGAGCGGATTCCAGGACCAGAGTATCGACGAAGGCGTGCGCAAGCGCACCGCCTACCAGAACGATC
GGCGTGCACGACTGGCATTGAACGTCGAGCGACAGGACGGCGGTATCCTGCAGATTCCGGTGGCCAG
CGATATGCTCGGCCATGAGGAGCACGAGCGTATCCAGCAGAACACCTTCCTGGCTGTGATGCCGCTG
GTCCGCCTGCCAACGCTGGGCAAGGCCGGTTATGGCGACCAGCTGCCCGCCGGCGCGCTACCGCGGG
CGGGACGGATCTACCTGTTCCAGGACGGCAAGTTGTGGCGCGAACTGGAATGTGATGGCAAGGGCAA
CCTGTTCGAAGTCGATCTCCTGCAGGGGCGCAGCCAGCGTGCGGACAAGCGTCCGGCCTTAGGCAAG
ACACAAGCGCTGATCCTGGTGCCGGTGCTGGTCAAGGGGCAGTTCGTGATCCCACGCTACACCATGG
CCTATAGCGAAACTCCCTGGCCTTGGTCGTACATCGACTGGCTGGAGGAGGACCCGCAGCGGGTCAA
CCGGCGCTGCCAGCAGATGGCGTCCGCTTGGAACGCCTCGGTGGCCAACCAGCACTGGAAAGCCTCC
ATCCATCAACCCGCGCTGGTCATTGATCATCACGCCCAGGGTTTGCGACCTCGCGACTTCAACGTCG
AGAGCGCGCTGGAAGACCCGGCGGAATTCACACCTGAGTTCGCCGCCTTTCGCGAAGAGTCGCTGGT
GTGCCAGTTGCAGCGACGCCAGCAGGAATTGGCGCCCCTGCTGAAGCAGGCTCCGCCCTCTGCGCTA
CCTACTCTGGAAGCCGGAGAGGACGTACTGGAAACCCTCAAGCTGCGTGGCCATCCCAACCTCATCG
GGCTGATGCTCGACGACTCGCTGTTCGCCTTGCGCCACGCTGCGGCGCAGGCGCGCCACTGCGCCGC
CTACTTGCGCAGCCTCAATGCACTGCTGCCGCACCGTCCCAACGGACGCTATGCACAGGTGCTGAGC
AACATGCTCGACGGCCCGCTCGCCAAGCTCAGGGGCGAGGTCGATCAGGCCGAACTGGACGAGGCGA
TCTTCGCCGAGGAGCGACAGTCTTGCCGAATCCACCTGACGCAGCAGGTCGAGCATCTGGTTGCCCT
GCTGGAAGGCCCCTTGCACCCGGTGTTGCAGGACTGGACCCACCAGTGCGACGAAGCCCTGCTGGAG
CCCTACAGCCTGATGAGCGAGGCACTGGCTGCGCTGAACCAGCTTCCCGACCGCTGCGACGCACTGT
ACAGCGGTACCGCCTACCGGGCGCTGGCGGCACATGTCGAGCGGGTGGTCAGCACGGTTCTGCAGGC
AAGCCACCCGCTTGGCGCCATGCTCCTGGCCAAGGACGAAGGACAACTTCCCGAGCCGGTTCGGCGC
CTGCAGGCGCTGCGCGATAGCCCGCGGACGCCGGACCCCGATGCAATGGGCCTCAGCACGCTGATGC
TGGGAGCCAGTCTGCTGGGCGAGGTCGACCAGCCCAGCGCCGGCAAGAGCCTCGCCTACTTCCTCGG
CGACCTGCTGGACGTGTTCGGCGCCAGCGTAGTCGAGCAACTCGGCCGGCTGTCCCAGGGCGCCACC
CAGATCCAGCTCGACCGCTTGTTCGCACCGACCTTCAATACTCTGAGCGCCCTCTCGGTGAAGATGA
AAGGTATCCGCCTGCTGCCCGACAGTCAGGTGCCGCTCGACATGGTTGTCGTCGGCGTGCGCGGAGC
CGGCCTGCGCAACGGTCTGACCGAGGTCGAGCGCCAGGAGCTGAGGCGCAAGAGCTATCGGCGCGCC
ATCGTTCAGGACGGTGCCGGCAATCCCCTGGCCGGCACCAGTCCCCGCGACACCGGCATGAGTCGCG
CCAACCTGCGCAACGTCATGGTGGTGGCGGTACCCAAGGATCACCCGGACCTGCTTGCCTACACGAA
ATTCCGTACGCAGTTAGGCACGTTGACCCAGGTGATGGAGAACACTCGCATCGTGCCGACGATGATG
CTGGGGTTTGCGATTTATAACTTGAATGTGCAGGTGCAGGCATACAGTGGCTTTGTAGACAGTGGAG
AAAAGCACAGAGGGACGATCGGGGCTGTCGGTGCAGTAATCGATTTAACAGCCGCTGGAGGAAGCCA
TGCAAAGCTGCTTTTCGGACCATCTACTGCAAAGTATCTAGAAACCCCACGTATATCGGTAGCCCAA
ATATCCCCTCGATGGGCCAGGAATCTAGAAGTTCAAACAGGCAGCCCTAAGTTAGGGTTGCTACGTG
GGCTTGGTGGCGCAGCCACACTATTCGGTGCAGGCATCAGTGTATGGGATGGCTACCGAGCTTTGAG
GCAGGGAGATAGCGATGCGGCTGCGGCCTACGGTGTGGCCGCAGTGGGTGGGGGCCTTTGGGGTGCC
TACGTCCTAGGATGGATAGTAAACCCTTATGCTTTGCTGGCTGGTGCGGTTTTGGCGATCGGAGGCA
CTGTGGTCGCTAATCTACTGACTGACAGCGATGCGGAAACCATCGTAAAGAAAGGCCCCTTCGGCCG
GCAATTCGCCGAGGCTGGCCTGCTCGATTCGCTGATGGGCCAGGACCAGCGCTTCGCCCATCTGAAA
GACCCGCAAACGGCCTATCGCCAATTGCTGGGAGTCCTCGGCCATCCGCGGGTCTTTGTCCATCGCC
TGGAAGACTGGCGCAAATTGGCGCCGGCGGCGCATCGATCTGTCTTGCAGGAAGCGGAACGGGGTCG
CCAAGCGGTCAGCCGCACTGCGCTATCCTGCATCGACCCCAAGTTGCAGGCGCTGGAGGCAAACGAT

TGGGCCGTGGTGCTGAGTTCCCCGCTCCTGGCCATGTTCGAGAATGGCCAGAAGGCGTTCCGCCTGG
TGGCCCAGGAGTTTCTCAGCAGCTTGCCGATCGATCCGGGCACCCTGTTCGGCGTCAAGCGCTACCA
TCGGGTCCCCGCGGGCCCCGCCAAGCTCGAAGCCTTGCCGTTGGATGCTGCCAGCGTGCTCTATGTG
CTGCCGGCCAGCCTGCCGATTCCGCAGTTGTCTCCTCGGGCCCGCTATAGCATGCGCATGACCCAGG
GTTTGAAGATCAGCGCACAGTTCGAACTCAATGCCGACCAGCCTGAGCAGCGGCTTGTCCTGCCTCA
ACCCAGCCCGAAGAGTTGGAGTGCATTCACATCCGCCAATCGGTACCTTCCCCCGGACGACTTGGGC
CCCCATGCTGCGCCACCTTATTGGTTGATAGAGAACAGTGAGTTCAACGTATGA

The VIR13 protein (SEQ ID NO:26) encoded by SEQ ID NO:25 is presented using the one-letter amino acid code in Table 15B.

Table 15B. Encoded VIR13 protein sequence (SEQ ID NO:26)

MSGFQDQSIDEGVRKRTAYQNDRRARLALNVERQDGGILQIPVASDMLGHEEHERIQQNTFLAVM
PLVRLPTLGKAGYGDQLPAGALPRAGRIYLFQDGKLWRELECDGKGNLFEVDLLQGRSQRADKRP
ALGKTQALILVPVLVKGQFVIPRYTMAYSETPWPWSYIDWLEEDPQRVNRRCQQMASAWNASVAN
QHWKASIHQPALVIDHHAQGLRPRDFNVESALEDPAEFTPEFAAFREESLVCQLQRRQQELAPLL
KQAPPSALPTLEAGEDVLETLKLRGHPNLIGLMLDDSLFALRHAAAQARHCAAYLRSLNALLPHR
PNGRYAQVLSNMLDGPLAKLRGEVDQAELDEAIFAEERQSCRIHLTQQVEHLVALLEGPLHPVLQ
DWTHQCDEALLEPYSLMSEALAALNQLPDRCDALYSGTAYRALAAHVERVVSTVLQASHPLGAML
LAKDEGQLPEPVRRLQALRDSPRTPDPDAMGLSTLMLGASLLGEVDQPSAGKSLAYFLGDLLDVF
GASVVEQLGRLSQGATQIQLDRLFAPTFNTLSALSVKMKGIRLLLPDSQVPLDMVVVGVRGAGLRN
GLTEVERQELRRKSYRRAIVQDGAGNPLAGTSPRDTGMSRANLRNVMVVAVPKDHPDLLAYTKFR
TQLGTLTQVMENTRIVPTMMLGFAIYNLNVQVQAYSGFVDSGEKHRGTIGAVGAVIDLTAAGGSH
AKLLFGPSTAKYLETPRISVAQISPRWARNLEVQTGSPKLGLLRGLGGAATLFGAGISVWDGYRA
LRQGDSDAAAAYGVAAVGGGLWGAYVLGWIVNPYALLAGAVLAIGGTVVANLLTDSDAETIVKKG
PFGRQFAEAGLLDSLMGQDQRFAHLKDPQTAYRQLLGVLGHPRVFVHRLEDWRKLAPAAHRSVLQ
EAERGRQAVSRTALSCIDPKLQALEANDWAVVLSSPLLAMFENGQKAFRLVAQEFLSSLPIDPGT
LFGVKRYHRVPAGPAKLEALPLDAASVLYVLPASLPIPQLSPRARYSMRMTQGLKISAQFELNAD
QPEQRLVLPQPSPKSWSAFTSANRYLPPDDLGPHAAPPYWLIENSEFNV

MUT14

A *Pseudomonas* bacterial mutant (MUT14) was made by transposon insertion in *a P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyochelin biosynthetic protein pchC (PA4229). This gene encodes the VIR14 nucleic acid (SEQ ID NO:27) shown in Table 16A.

Table 16A. VIR14 Nucleotide Sequence (SEQ ID NO:27)

ATGAGCGCCGCCTGGGTCCGGCCGTTCCGCCTGACGCCGATGCCGCGCCTGCGCCTGGCCTGCTTCC
CCCATGCAGGCGGCAGCGCCAGCTTCTTCCGTAGCTGGAGCGAACGCCTGCCGCCAGACATCGACCT
GCTTGCCCTGCAGTACCCGGGTCGCGAGGACCGCTTCAACGAGGCGCCGGCCACCCGCCTGGAGGAC
CTCGCCGACGGCGCCGCCCTCGCCCTGCGCGATTTCGCCGACGCGCCCCCTGGCGCTGTTCGGCCACA
GTCTCGGCGCGGCGCTGGCCTACGAAACCGCCCTGCGCCTGGAAAGCGCCGGCGCGCCGCTGCGCCA
CCTGTTCGTCTCCGCCCATCCGGCACCGCACCGGCAACGCGGCGGCGCGTTGCACCGCGGCGACGAG
GCGGCGCTGCTGGAGGACGTCCGCCGCCAGGGTGGCGCCAGCGAGCTACTCGAGGACGCCGACCTGC
GCGCGCTGTTCCTGCCGATCCTGCGCGCCGACTACCAGGCGATCGAGACCTACCGACGGGCGCAGCC

CATCGCCCTGGCCTGCGCCCTCGACGTCCTCCTCGGCGAGCACGACGAGGAAGTCAGCGCCGCCGAG
GCGCAGGCCTGGAGCGACGCCAGCCGGACTCCCGCCAGGCTGCGGCGCTTTCCTGGCGGCCACTTCT
ACCTGAGCGAGGGGCGCGACGCGGTGATCGAGCACCTGCTGCGCCGCCTCGCACATCCCGACGCCCT
TTCCCGAGAGGTTGCATGA

The VIR14 protein (SEQ ID NO:28) encoded by SEQ ID NO:27 is presented using the one-letter amino acid code in Table 16B.

Table 16B. Encoded VIR14 protein sequence (SEQ ID NO:28)

MSAAWVRPFRLTPMPRLRLACFPHAGGSASFFRSWSERLPPDIDLLALQYPGREDRFNEAPATRLEDL
ADGAALALRDFADAPLALFGHSLGAALAYETALRLESAGAPLRHLFVSAHPAPHRQRGGALHRGDEAA
LLEDVRRQGGASELLEDADLRALFLPILRADYQAIETYRRAQPIALACALDVLLGEHDEEVSAAEAQA
WSDASRTPARLRRFPGGHFYLSEGRDAVIEHLLRRLAHPDALSREVA

MUT15

A *Pseudomonas* bacterial mutant (MUT15) was made by transposon insertion in *a P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding dihydroaeruginoic acid synthetase pchE (PA4226). This gene encodes the VIR15 nucleic acid (SEQ ID NO:29) shown in Table 17A.

Table 17A. VIR15 Nucleotide Sequence (SEQ ID NO:29)

ATGGATCTGCCCCCCGATTCCCGTACCGCCCTGCGCGACTGGCTGACCGAGCAGCTCGCCGACCTGC
TCGGCGAACCGCTTGCTGACGTGCGCGCCCTGGCGGACGACGACGACCTGCTGGGCTGCGGCCTCGA
CTCGATCCGCCTGATGTACCTGCAGGAACGCCTGCGCGCGCGTGGCTCGACGCTGGACTTCGCCCAG
TTGGCGCAGCGCCCCTGCCTGGGGGCCTGGCTCGACCTGCTGGCCTGCGCGGACCGGCTGTCCGCCC
CGGCAACGGTCGCGCTGCCGACGGCGCAGGATCGCGATCAGCCGTTCGAGCTGTCTTCCGTGCAGCA
GGCCTACTGGCTGGGACGTGGCGCCGGCGAGGTGCTGGGCAACGTCAGCTGCCATGCCTTTCTGGAA
TTCCGCACGCGGGATGTCGACCCGCAGCGCCTGGCCGCGGCGGCGGAGTGCGTGCGTCAACGCCACC
CGATGTTGCGGGCGCGCTTCCTCGACGGTCGCCAGCAGATCCTTCCGACGCCGCCGCTGTCCTGCTT
CGACCTGCAGGACTGGCGCACCTTACAGGTGGACGAGGCCGAGCGCGACTGGCAGGCGCTGCGCGAC
TGGCGCGCCCATGAATGCCTGGCGGTGGAGCGCGGCCAGGTGTTCCTGCTCGGGCTGGTGCGCATGC
CGGGCGGCGAGGATCGCCTCTGGCTGAGTCTCGACCTGCTTGCCGCCGATGTCGAAAGCCTGCGCCT
GCTGCTGGCCGAACTGGGCGTTGCCTACCTGGCGCCGGAGCGCCTGGCGGAGCCGCCGGCGCTGCAT
TTCGCCGACTACCTGGCGCACCGTGCGGCGCAACGCGCCGAGGCCGCGGCGCGGGCCCGCGACTACT
GGCTGGAACGCCTGCCGCGCTTGCCGGACGCGCCGGCCCTGCCGTTGGCCTGCGCGCCGGAAAGCAT
CCGCCAGCCGCGCACCCGGCGCCTGGCATTCCAGCTTTCCGCCGGCGAGAGCCGGCGCCTGGAGCGT
CTTGCCGCGCAGCATGGCGTGACCTTGTCCAGCGTGTTCGGCTGCGCCTTCGCGCTGGTCCTGGCGC
GCTGGAGCGAAAGCGCGGAATTTCTCCTCAACGTGCCGTTGTTCGATCGGCATGCCGACGACCCGCG
TATCGGCGAGGTGATCGCCGACTTCACCACCCTGTTGCTGCTGGAGTGCCGGATGCAGGCCGGGGTG
TCCTTCGCCGAGGCGGTGAAGAGCTTCCAGCGCAACCTCCACGGAGCCATCGACCACGCCGCATTCC
CCGCCCTGGAGGTGCTCCGCGAGGCGCGCCGGCAGGGCCAGCCACGCTCGGCGCCGGTGGTGTTCGC
CAGCAACCTGGGCGAGGAGGGCTTCGTCCCGGCGGCCTTCCGCGACGCTTTCGGCGATCTCCACGAC
ATGCTCTCGCAGACCCCGCAGGTCTGGCTCGACCACCAGCTCTACCGGGTGGGCGACGGTATCCTGC
TGGCCTGGGATAGCGTCGTCGGCCTGTTCCCCGAAGGTCTGCCGGAAACCATGTTCGAAGCCTACGT
GGGGCTGCTCCAGCGTCTCTGCGACAGCGCCTGGGGGCAGCCCGCCGATCTGCCGTTGCCCTGGGCG

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CAGCAGGCGCGCCGGGCCCTGCTCAACGGCCAGCCGGCATGCGCCACGGCGCGCACCCTGCATCGCG
ACTTCTTCCTTCGCGCCGCCGAGGCGCCGGATGCCGACGCGCTGCTCTATCGCGACCAACGTGTCAC
CCGCGGCGAACTGGCCGAGCGTGCGCTGCGCATCGCCGGCGGCCTGCGCGAAGCCGGGGTGCGCCCT
GGCGACGCGGTCGAGGTCAGCCTGCCGCGCGGACCGCAGCAGGTCGCGGCGGTATTCGGCGTGCTCG
CCGCAGGCGCCTGCTACGTGCCGCTGGACATCGACCAGCCGCCCGCACGGCGGCGCCTGATCGAAGA
GGCCGCCGGGGTATGCCTGGCGATCACCGAGGAGGACGATCCGCAGGCCTTGCCGCCGCGCCTGGAT
GTCCAGCGCCTGCTGCGCGGCCCGGCGCTGGCCGCCCCCGTGCCGCTGGCGCCGCAGGCGAGTGCCT
ATGTGATCTACACCTCGGGCTCCACCGGGGTGCCCAAGGGCGTCGAGGTCAGCCACGCGGCGGCGAT
CAATACCATCGACGCGCTGCTCGACCTGCTGCGGGTGAACGCATCGGATCGCTTGCTGGCGGTCTCC
GCGCTGGACTTCGATCTGTCGGTCTTCGACCTGTTCGGCGGCCTCGGCGCCGGTGCCAGCCTGGTCC
TGCCGGCCCAGGAACAGGCGCGCGATGCCGCTGCCTGGGCGGAGGCTATCCAGCGGCATGCGGTGAG
CCTGTGGAACTCGGCGCCGGCCTTGCTGGAGATGGCCCTCAGCCTGCCGGCGAGCCAGGCCGACTAT
CGCAGTCTGCGGGCGGTGCTGCTGTCCGGCGACTGGGTGGCCCTGGACCTGCCCGGCCGCCTGCGCC
CACGTTGTGCCGAAGGCTGCCGCCTGCATGTGCTGGGTGGCGCTACCGAAGCGGGCATCTGGTCGAA
CCTGCAGAGCGTCGATACGGTGCCGCCGCACTGGCGTTCGATTCCCTACGGCCGGCCATTGCCGGGA
CAGGCCTACCGGGTGGTCGACACCCACGGGCGCGACGTGCCGGACCTGGTGGTCGGCGAGCTGTGGA
TCGGCGGCGCCAGCCTGGCCCGCGGCTATCGCAACGATCCCGAACTCAGCGCCCGGCGTTTCGTCCA
CGATGCCCAGGGCCGCTGGTATCGCACCGGCGATCGCGGTCGCTACTGGGGCGACGGTACCCTGGAA
TTCCTCGGTCGGGTCGACCAGCAGGTGAAAGTGCGCGGCCAGCGCATCGAGTTGGGCGAGGTGGAGG
CCGCGCTGTGCGCCCAGGCTGGCGTGGAGAGCGCCTGCGCGGCGGTGCTCGGCGGTGGCGTGGCGAG
CCTCGGCGCGGTGCTGGTACCGCGCCTGGCGCCACGGGCCGAAGGCTCCATGGATCTACCGGCCGCA
CAGCCCTTCGCCGGCCTGGCAGAGGCCGAGGCGGTACTCACCCGGGAAATCCTCGGCGCGCTGCTGG
AGGCGCCGCTGGAGCTAGACGACGGTTTGCGCCGGCGCTGGCTGGACTGGCTAGCGGACTCCGCCGC
CAGCGCGCTGCCGTCGCTCGACGAGGCGTTGCGCCGGCTCGGCTGGCAGGCCGCGGGGCTGACCGCG
ATGGGCAACGCTCTGCGCGGCCTGCTCGCCGGCGAACAGGCGCCGGCCGCGCTGCTCCTCGATCCCT
GGCTGGCGCCGCAGGCGGTGGCCGCGCGCCTGCCGGACGGCCGCGAGGCCCTGGCGCGCCTGCTCGA
AGCGCTGCCGACGCCGGCTGCCGGCGAACGCCTGCGGGTGGCGGTGCTGGATACCCGCGCCGGGCTC
TGGCTCGACCAGGGCATGGCCTCGCTGTTGCGCCCAGGGCTGGAACTGACCCTCTTCGAACGCAGCC
GCGTCCTCCTCGACGCCGCCGCCACCCGCTTGCCGGAACGGATCGTGGTGCAGGCGCTGGACGACGG
CCTGCTACCTGCCGAGCACCTCGGTCGCTACGACCGGGTGATCAGCTTCGCCGCGCTGCACGCCTAC
GAGGCCAGCCGCGAAGGCCTGGCGCTGGCGGCGGCGCTGCTGCGCCCGCAGGGCCGCCTGTTGCTGG
TGGACCTGCTATGCGAGTCGCCACTGGCGCTGCTCGGTGCGGCCTTGCTCGACGACCGGCCGCTGCG
CCTGGCGGAGCTGCCGAGCCTGTTGGCCGATCTCGCCGCTGCGGGACTGGCGCCGCGTTGCCTGTGG
CGCAGCGAGCGGATCGCCCTGGTCGAGGCGCTGGCACCGGGACTCGGGCTCGACGCCGCCGCGCTCC
AGGCCGGCCTGGAGCAACGCCTGCCCCAGGCGATGCGGCCCGAACGCCTGTGGTGCCTGCCAAGCCT
GCCGTTGAACGGCAATGGCAAGGTCGATCGTCGCCGCCTGGCCGAGAGCATGACCCGCGCACTCGGC
GAGTGTCGTCACGAGCCCTCGGCGGAGGAGCCGCTGGAAGCCCATGAGCAAGCGCTGGCCGAGTGCT
GGGAAGCGGTTCTCAAACGCCCGGTGCGTCGTCGCGAGGCGAGCTTCTTCAGCCTCGGCGGCGACAG
CCTGCTGGCGACCCGCCTGCTGGCCGGCATACGTGAGCGTTTCGGCGTACGCCTGGGCATGGCCGAC
TTCTATCGCCAGCCGACCCTGGCCGGTCTTGCCCGCCACTTGCAGGTGCAGACCGTCGAAATCGAGG
AAACCCAACTGGAAGAGGGCGTGCTATGA
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The VIR15 protein (SEQ ID NO:30) encoded by SEQ ID NO:29 is presented using the one-letter amino acid code in Table 17B.

Table 17B. Encoded VIR15 protein sequence (SEQ ID NO:30)

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MDLPPDSRTALRDWLTEQLADLLGEPLADVRALADDDDLLGCGLDSIRLMYLQERLRARGSTLDFAQL
AQRPCLGAWLDLLACADRLSAPATVALPTAQDRDQPFELSSVQQAYWLGRGAGEVLGNVSCHAFLEFR
TRDVDPQRLAAAAECVRQRHPMLRARFLDGRQQILPTPPLSCFDLQDWRTLQVDEAERDWQALRDWRA
HECLAVERGQVFLLGLVRMPGGEDRLWLSLDLLAADVESLRLLLAELGVAYLAPERLAEPPALHFADY
LAHRAAQRAEAAARARDYWLERLPRLPDAPALPLACAPESIRQPRTRRLAFQLSAGESRRLERLAAQH
GVTLSSVFGCAFALVLARWSESAEFLLNVPLFDRHADDPRIGEVIADFTTLLLLECRMQAGVSFAEAV
KSFQRNLHGAIDHAAFPALEVLREARRQGQPRSAPVVFASNLGEEGFVPAAFRDAFGDLHDMLSQTPQ
VWLDHQLYRVGDGILLAWDSVVGLFPEGLPETMFEAYVGLLQRLCDSAWGQPADLPLPWAQQARRALL
NGQPACATARTLHRDFFLRAAEAPDADALLYRDQRVTRGELAERALRIAGGLREAGVRPGDAVEVSLP
RGPQQVAAVFGVLAAGACYVPLDIDQPPARRRLIEEAAGVCLAITEEDDPQALPPRLDVQRLLRGPAL
AAPVPLAPQASAYVIYTSGSTGVPKGVEVSHAAAINTIDALLDLLRVNASDRLLAVSALDFDLSVFDL
FGGLGAGASLVLPAQEQARDAAAWAEAIQRHAVSLWNSAPALLEMALSLPASQADYRSLRAVLLSGDW
VALDLPGRLRPRCAEGCRLHVLGGATEAGIWSNLQSVDTVPPHWRSIPYGRPLPGQAYRVVDTHGRDV
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PDLVVGELWIGGASLARGYRNDPELSARRFVHDAQGRWYRTGDRGRYWGDGTLEFLGRVDQQVKVRGQ
RIELGEVEAALCAQAGVESACAAVLGGGVASLGAVLVPRLAPRAEGSMDLPAAQPFAGLAEAEAVLTR
EILGALLEAPLELDDGLRRRWLDWLADSAASALPSLDEALRRLGWQAAGLTAMGNALRGLLAGEQAPA
ALLLDPWLAPQAVAARLPDGREALARLLEALPTPAAGERLRVAVLDTRAGLWLDQGMASLLRPGLELT
LFERSRVLLDAAATRLPERIVVQALDDGLLPAEHLGRYDRVISFAALHAYEASREGLALAAALLRPQG
RLLLVDLLCESPLALLGAALLDDRPLRLAELPSLLADLAAAGLAPRCLWRSERIALVEALAPGLGLDA
AALQAGLEQRLPQAMRPERLWCLPSLPLNGNGKVDRRRLAESMTRALGECRHEPSAEEPLEAHEQALA
ECWEAVLKRPVRRREASFFSLGGDSLLATRLLAGIRERFGVRLGMADFYRQPTLAGLARHLQVQTVEI
EETQLEEGVL

MUT16

A *Pseudomonas* bacterial mutant (MUT16) was made by transposon insertion in *a P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyochelin synthetase pchF (PA4225). This gene encodes the VIR16 nucleic acid (SEQ ID NO:31) shown in Table 18A.

Table 18A. VIR16 Nucleotide Sequence (SEQ ID NO:31)

ATGAGCCTCGGCGAACTGCTGGAAACCTGCCGCAGCCGGCGCATCGAACTCTGGAGCGAGGCGGGCC
GCCTGCGCTATCGCGCCCCCCAGGGTGCCCTCGACGCCGGCCTCGCCGAGCGCCTGCGGGCCGAGCG
CGAGGCCCTGCTGGAACACCTGGAAGGCGGCCCTGGCTGGCGCGCCGAACCCGACATGGCCCACCAG
CGCTTCCCGCTGACCCCGGTGCAGGCCGCCTACGTGCTGGGCCGCCAGGCGGCCTTCGACTACGGCG
GTAACGCCTGCCAGCTGTACGCCGAGTACGACTGGCCGGCCGACACCGATCCGGCGCGCCTGGAGGC
GGCCTGGAACGCCATGGTCGAGCGCCACCCGATGCTGCGCGCGGTGATCGAGGACAACGCCTGGCAG
CGCGTGCTGCCCGAGGTGCCCTGGCAGCGGCTGACCGTGCATGCCTGCGCGGGGCTCGACGAGGCCG
CTTTCCAGGCGCACCTGGAGCGGGTCCGCGAACGCCTCGACCACGCCTGCGCGGCGCTCGACCAGTG
GCCGGTCCTGCGCCCCGAGCTGAGTATCGGCCGGGATGCCTGCGTACTGCACTGCTCGGTGGATTTC
ACCCTGGTCGACTACGCCAGCCTGCAATTGCTGCTTGGCGAATGGCGCCGCCGCTATCTCGATCCGC
AATGGACGGCGGAACCGCTGGAGGCGACCTTCCGCGACTATGTCGGCGTCGAGCAGCGCCGACGCCA
GTCGCCAGCCTGGCAGCGCGACCGCGACTGGTGGCTGGCGCGTCTCGACGCGCTACCGGGGCGTCCC
GACCTGCCGCTGCGGGTGCAGCCGGACACCCGGTCCACGCGCTTCCGGCACTTCCACGCGCGCCTCG
ACGAGGCCGCCTGGCAGGCGCTCGGCGCGCGCCGGCGAACACGGCCTGAGCGCTGCCGGCGTGGC
CTTGGCGGCCTTCGCCGAGACCATCGGTCGCTGGAGCCAGGCACCGGCGTTCTGTCTCAACCTGACG
GTACTCAACCGGCCGCCGCTGCATCCGCAGCTGGCGCAGGTGCTCGGTGACTTCACCGCGCTCAGCC
TGCTGGCAGTGGACAGCCGCCACGGCGACAGTTTCGTCGAGCGTGCCCGACGCATCGGCGAGCAGAT
GTTCGACGACCTCGACCACCCGACCTTCAGCGGCGTCGACCTGCTGCGCGAACTGGCGCGCCGGCGT
GGTCGCGGCGCCGATCTGATGCCGGTGGTGTTCACCAGTGGCATCGGCAGCGTGCAGCGCCTGCTCG
GCGATGGCGAGGCGCCGCGCGCGCCACGCTACATGATCAGCCAGACCCCGCAGGTCTGGCTGGACTG
CCAGGTCACCGACCAGTTCGGCGGCCTGGAGATCGGCTGGGACGTACGCCTCGGGTTGTTCCCCGAG
GGCCAGGCGGAAGCCATGTTCGACGACTTCGTCGGGCTGCTCCGGCGCCTGGCGCAGAGCCCGCGCG
CCTGGACCGACGGCGATGCCACGGAACCCGTCGAGGCGCCGCCGCAGGCGTTGCCCGGTAGTGCCCG
GAGCATCGCCGCCGGTTTCGCCGAGCGTGCCCTGCTGACCCCCGACGCCACGGCGATCCACGATGCC
GCCGGCAGCTACAGCTACCGCCAGGTCGCCCAGCACGCCAGCGCCCTGCGCCGCGTCCTGGAAGCGC
ACGGCGCGGGCCGTGGCCGGCGGGTCGCGGTGATGCTGCCGAAAAGCGCCGCGCAATTGGTCGCGGT
GATCGGCATCCTCCAGGCCGGCGCCGCCTATGTGCCGGTGGACATCCGCCAGCCTCCGCTGCGGCGC
CAGGCGATCCTCGCCAGCGCCGAAGTGGTCGCGCTGGTCTGCCTGGAAAGCGATGTCCCGGACGTCG
GCTGCGCCTGCGTGGCCATCGACCGGCTGGCCGCCGACAGCGCCTGGCCGCCACCGCCCGCGGCGGA
GGTGGCGGCGGACGACCTCGCCTACGTGATCTACACCTCCGGCTCCACCGGCACGCCAAAGGGCGTG
ATGCTCAGCCATGCGGCGGTGAGCAACACGCTGCTCGACATCAACCAGCGCTACGGCGTCGACGCCA
ACGACCGCGTCCTCGGCCTCGCCGAGCTGAGCTTCGACCTCTCGGTCTACGACTTCTTCGGCGCCAC
CGCGGCGGGGGCCCAGGTGGTCCTCCCGGACCCGGCGCGCGGCAGCGATCCATCGCACTGGGCGGAA
CTGCTGGAACGCCACGCCATCACCCTGTGGAACTCGGTGCCGGCCCAAGGCCAGATGCTCATCGATT
ACCTGGAGAGCGAGCCGCAACGTCACCTGCCGGGACCGCGCTGCGTGCTCTGGTCCGGTGACTGGAT

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TCCGGTCAGCCTGCCGACCCGCTGGTGGCGGCGCTGGCCGGACAGCGCGCTGTTCAGCCTGGGCGGC
GCCACCGAGGCGGCGATCTGGTCGATCGAGCAGCCGATCCGCCCGCAGCACACCGAGCTGGCCAGCA
TCCCTTATGGCCGTGCCCTGCGCGGGCAGAGCGTGGAAGTCCTGGATGCCCGCGGGCGGCGCTGCCC
GCCGGGCGTGCGCGGCGAGATCCATATCGGCGGGGTGGGCCTGGCGCTCGGCTACGCCGGCGATCCG
CAGCGCACCGCCGAACGCTTCGTCCGTCACCCCGATGGCCGTCGCCTGTATCGCACCGGCGACCTCG
GCCGCTACCTGGCCGACGGCAGCATCGAGTTCCTCGGCCGCGAGGACGACCAGGTGAAGATTCGCGG
CCACCGCATCGAACTGGCCGAACTGGACGCCGCGCTGTGCGCTCATCCGCAGGTCAACCTGGCGGCC
ACCGTGGTGCTCGGCGAGACCCACGAGCGCAGCCTGGCCAGCTTCGTCACCCTGCATGCGCCGGTGG
AGGCTGGCGAGGATCCGCGTACGGCGCTCGACGCGGTGCGCCAGCGGGCGGCCCAGGCCTTGCGCCG
CGACTGGGGCAGCGAGGAGGGCATCGCCGCGGCGGTGGCCGCACTCGACCGTGCCTGCCTCGCCTCG
TTGGCCGCCTGGCTGGCCGGCAGCGGTCTGTTCGCCAGTGCGACGCCGCTGGACTTAGCCACCCTGT
GCCAGCGCCTGGGTATCGCCGAGGCGCGCCAGCGCCTGCTGCGCCACTGGTTGCGCCAACTGGAGGA
GGGCGGCTACCTGCGCGCCGAGGGCGAGGGCTGGCTGGGCTGCGCCGAGCGTCCCGCGCAGAGTCCG
GAGGACGCCTGGACGGCGTTCGCCGGCTGCGCGCCGGCGGCGCTCTGGCCGGCCGAGCTGGTCGCCT
ACCTGCGTGACAGCGCGCAATCCCTCGGCGAGCAACTGGCCGGGCGGATCAGCCCGGCGGCGCTGAT
GTTCCCGCAGGGCTCGGCGCGCATCGCCGAGGCCATGTACAGCCAGGGCCTGCATGCCCAGGCGCTG
CACGAGGCCATGGCCGAGGCCATCGCCGCCATCGTCGAGCGCCAGCCGCAACGGCGCTGGCGCCTGC
TGGAGCTTGGCGCCGGCACCGCCGCCGCCAGCCGCACGGTGATCGCCCGGTTGGCGCCGCTGGTGCA
GCGAGGGGCGGAGGTGGACTACCTGTTCACCGACGTTTCCAGCTACTTCCTCGCCGCCGCCCGCGAG
CGCTTCGCCGACCAGCCGTGGGTACGCTTCGGCCGCTTCGACATGAACGGCGATCTTCTCGACCAGG
GCGTGGCGCCGCACTCGGTGGATATCCTGCTCAGCTCCGGGGCCTTGAACAACGCGCTGGACACCCC
GGCGCTGCTGGCCGGCCTGCGCGAGTTGCTGAGCGCCGACGCCTGGCTGGTGATCCAGGAACTGACG
CGCGAGCACAACGAGATCAGCGTCAGCCAGAGCCTGATGATGGAAAACCCGCGCGACCTCCGCGACG
AGCGCCGCCAACTGTTCGTCCACACCGGGCAATGGCTGGAGTGGCTGGCGGCACAGGGTGGCGACCT
GGCTTGTGGGGTGGTGCCGCCGGGCAGCGCTCTCGACCTGCTTGGCTACGATGTCCTGCTGGCTCGC
TGCAAGACCGACCGCGCCCGCCTGGAGCCGGCCGAGCTGCTGGCCTTCGTCGAAGCGCGGGTGCCGC
GCTACATGCTCCCGGCGCAGTTGCGCGTGCTCGAACGCCTGCCGGTCACCGGCAACGGCAAGATCGA
CCGCAAGGCCCTGACCGGCTTTGCCCGCCAGCCCCAGGCGGACCTTCGGCATGGCGTCGCGCAGGCA
CCGGCCGACGAACTGGAGAATGCGCTGCTGGCACTCTGGCGGGAGGTGCTGGACAACCCGTCGCTGG
GCGTCGAGCAAGACTTCTTCGGGGCCGGCGGCGACTCGCTGTTGATCGCCCAGTTGATCGCCCGTTT
GCGCGAACGACTGGAAAGCGCCCGTCGGCATCCGTTCGATCGCCTGCTACGCTGGGCGCTCAGCCAG
CCGACGCCGCGCGGCCTGGCCGAACGCCTGCGCAGCGCGCCGGAAGAGGGCCGTGGGCCAGCCCTGG
CCGCGGCGCGCGGCGTCGCCCCGGCGCCGGCCGGCATGTCGCGCGCACCGCTCGCCGAGGGCGCGGT
GGCGCTCGACCCGCTGGTGCGCCTGGTGCCCGGCGAGGGCGTGCCGCGGGTGCTGGTCCACGAAGGC
CTCGGCACGCTACTGCCGTACCGCCCGCTGCTTCGCGCCCTGGGTGAGGGGCGGCCGTTGCTGGGGC
TGGCCGTGCATGACAGCGACGCCTACCTGGCGATCCCCGCCGAGCATCTCAACGCCTGCCTCGGCCG
CCGCTACGCCGAGGCGCTCCATCGCGCCGGGCTACGCGAGGTCGACCTGCTCGGCTACTGCTCCGGC
GGGCTGGTCGCCCTGGAGACCGCCAAGTCCCTGGTCCAGCGCGGGGTGCGCGTGCGCCAACTGGATA
TCGTCTCCAGCTACCGGATTCCCTACCGGGTGGACGACGAGCGCCTGCTGTTGTTCAGCTTCGCCGC
GACCCTCGGCCTGGATACCGCGGCGCTCGGCTTCCCCGCGCCGGAACGTCTCGGCCAGGCGGTGCAG
GCGGCGCTCGCGCAGACACCGGAGCGCCTGGTCGCCGAGGCGCTGGCGGGGCTGCCGGGCCTGGCCG
ATCTCGTCGCCCTGCGCGGCCGCGTGCTACAGGCGGCCAGCGGTAGCGCCGACGCCGTCAGCGTCGA
ACGCGACACCCTCTACCGGCTGTTCTGTCACTCGGTGCGTGCCAGCCAGGCCGAGGCGCCGGAGCCC
TACGTCGGCGCGCTGCGGCTGTTCGTGCCGGACGCCGGCAACCCATTGGTGCCGCGCTACGCCGAGG
CTCTGGAGACCCAATGGCGGGCCGCCGCGCTTGGCGCGTGCGGCATCCACGAGGTGCCCGGCGGGCA
CTTCGACTGCCTGGGCGAAGCCCTGGCGCAATCCTTGTCGAAACCCATGCCAGAGGAGGCGAGCCGA
TGA
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The VIR16 protein (SEQ ID NO:32) encoded by SEQ ID NO:31 is presented using the one-letter amino acid code in Table 18B.

Table 18B. Encoded VIR16 protein sequence (SEQ ID NO:32)

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MSLGELLETCRSRRIELWSEAGRLRYRAPQGALDAGLAERLRAEREALLEHLEGGPGWRAEPDMA
HQRFPLTPVQAAYVLGRQAAFDYGGNACQLYAEYDWPADTDPARLEAAWNAMVERHPMLRAVIED
NAWQRVLPEVPWQRLTVHACAGLDEAAFQAHLERVRERLDHACAALDQWPVLRPELSIGRDACVL
HCSVDFTLVDYASLQLLLGEWRRRYLDPQWTAEPLEATFRDYVGVEQRRRQSPAWQRDRDWWLAR
LDALPGRPDLPLRVQPDTRSTRFRHFHARLDEAAWQALGARAGEHGLSAAGVALAAFAETIGRWS
QAPAFCLNLTVLNRPPLHPQLAQVLGDFTALSLLAVDSRHGDSFVERARRIGEQMFDDLDHPTFS
GVDLLRELARRRGRGADLMPVVFTSGIGSVQRLLGDGEAPRAPRYMISQTPQVWLDCQVTDQFGG
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LEIGWDVRLGLFPEGQAEAMFDDFVGLLRRLAQSPRAWTDGDATEPVEAPPQALPGSARSIAAGF
AERALLTPDATAIHDAAGSYSYRQVAQHASALRRVLEAHGAGRGRRVAVMLPKSAAQLVAVIGIL
QAGAAYVPVDIRQPPLRRQAILASAEVVALVCLESDVPDVGCACVAIDRLAADSAWPPPPAAEVA
ADDLAYVIYTSGSTGTPKGVMLSHAAVSNTLLDINQRYGVDANDRVLGLAELSFDLSVYDFFGAT
AAGAQVVLPDPARGSDPSHWAELLERHAITLWNSVPAQGQMLIDYLESEPQRHLPGPRCVLWSGD
WIPVSLPTRWWRRWPDSALFSLGGATEAAIWSIEQPIRPQHTELASIPYGRALRGQSVEVLDARG
RRCPPGVRGEIHIGGVGLALGYAGDPQRTAERFVRHPDGRRLYRTGDLGRYLADGSIEFLGREDD
QVKIRGHRIELAELDAALCAHPQVNLAATVVLGETHERSLASFVTLHAPVEAGEDPRTALDAVRQ
RAAQALRRDWGSEEGIAAAVAALDRACLASLAAWLAGSGLFASATPLDLATLCQRLGIAEARQRL
LRHWLRQLEEGGYLRAEGEGWLGCAERPAQSPEDAWTAFAGCAPAALWPAELVAYLRDSAQSLGE
QLAGRISPAALMFPQGSARIAEAMYSQGLHAQALHEAMAEAIAAIVERQPQRRWRLLELGAGTAA
ASRTVIARLAPLVQRGAEVDYLFTDVSSYFLAAARERFADQPWVRFGRFDMNGDLLDQGVAPHSV
DILLSSGALNNALDTPALLAGLRELLSADAWLVIQELTREHNEISVSQSLMMENPRDLRDERRQL
FVHTGQWLEWLAAQGGDLACGVVPPGSALDLLGYDVLLARCKTDRARLEPAELLAFVEARVPRYM
LPAQLRVLERLPVTGNGKIDRKALTGFARQPQADLRHGVAQAPADELENALLALWREVLDNPSLG
VEQDFFGAGGDSLLIAQLIARLRERLESARRHPFDRLLRWALSQPTPRGLAERLRSAPEEGRGPA
LAAARGVAPAPAGMSRAPLAEGAVALDPLVRLVPGEGVPRVLVHEGLGTLLPYRPLLRALGEGRP
LLGLAVHDSDAYLAIPAEHLNACLGRRYAEALHRAGLREVDLLGYCSGGLVALETAKSLVQRGVR
VRQLDIVSSYRIPYRVDDERLLLFSFAATLGLDTAALGFPAPERLGQAVQAALAQTPERLVAEAL
AGLPGLADLVALRGRVLQAASGSADAVSVERDTLYRLFCHSVRASQAEAPEPYVGALRLFVPDAG
NPLVPRYAEALETQWRAAALGACGIHEVPGGHFDCLGEALAQSLSKPMPEEASR

MUT17

A *Pseudomonas* bacterial mutant (MUT17) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding putative ATP-binding component of the ABC transporter, pchH (PA4223). This gene encodes the VIR17 nucleic acid (SEQ ID NO:33) shown in Table 19A.

Table 19A. VIR17 Nucleotide Sequence (SEQ ID NO:33)

GTGACCCCGGTGCTGTGGCGCCTGCTGCGCACCTATCGCTGGCGGCTGGCGGCGGCCATGGGGTTGC
AGGCCCTGGCCGGGCTCTGCTCGCTGTTGCCCTGGATGCTTCTCGCCTGGCTCGCCGAGCCGCTGGC
GCGCGGCCAGGCGCAGCCGGCCCTGCTGGCCCTGGTGCTGCTGGCGGTGCTGGCCTGGCTGGGCTGC
CAGGCGCTGGCCGCGCACCTGGCCCACCGGGTCGACGCGGACCTCTGCAACGACCTGCGCCTGCGCC
TGCTGGCGCACCTGCAACGGCTGCCGCTGGACTGGTTCGGTCGCCAGGGCCCGGACGGCGTGGCGCG
CCTCGTGGAGCAGGACGTGCGGGCCCTGCACCAACTGATCGCGCACGCTCCCAACGATCTCAGCAAC
CTGTTGGTGGTGCCGCTCGTCGCGTTGCTCTGGCTGGCCTGGCTGCACCCCTGGCTGCTGCTGTTCT
GCCTGCTGCCGCTGGTGCTGGCCGCCGGCTTCCTGCTGCTGCGCTCGGCGCGCTACCGCGACCT
GGTGCTGCGGCGCAACGCCGCGCTGGAAAGGCTCTCGGCGGACTATGGCGAATTCGCCCACAACCTG
CTGCTGGCCCGACAGTACCCCGGCGCCGGCATACAACAGGGCGCCGAGGCGTCGGCGGCGGCCTTCG
GCGAAGCGTTCGGCGCCTGGGTGAAGCGGGTCGGCCACCTCGCCGCGCTGGTCTACGTGCAGTTGTC
GACGCCCTGGCTGCTGGCCTGGGTCCTGCTCGGCGCGCTGGCCCTGGATGCCCTCGGCGTGCCGCTG
GCGCTCGGCCAGGCCTGTGCCTTCCTGCTCCTGCTGCGGGCCTTGGCTGCCCCGGTGCAGGCGCTCG
GCCACGGCGGCGACGCGCTGCTGGGCGCGCGCGCCGCCGCCGAGCGCCTGCAGCAGGTGTTCGACCA
GGCGCCGCTGGCCGAGGGCCGCTCGACCCGCGAGCCGGTCGATGGCGCGGTGGCGCTGCACGGCCTG
GGCCATGCCTATGAAGGCGTGGAGGTCCTGGCCGATATCGATCTGGAGCTGGAGGATGGCAGCCTGG
TGGCCCTGGTCGGTCCCTCGGGCTCCGGCAAGAGCACCCTGCTGCACCTGCTGGCGCGCTACATGGA
CGCGCAGCGCGGCGAACTGGAGGTTGGCGGCCTGGCACTGAAGGACATGCCTGATGCCGTGCGCCAT
CGGCATATCGCGCTGGTCGGCCAGCAGGCGGCGGCGCTGGAGATATCCCTGGCCGACAACATTGCCC
TGTTCCGCCCCGATGCCGATCTCCAGGAGATTCGCCAGGCGGCCCGTGACGCCTGCCTCGACGAGCG
CATCATGGCCCTGCCGCGTGGCTACGACAGCGTGCCGGGACGCGACCTGCAACTGTCCGGCGGCGAA
CTGCAACGACTGGCCCTGGCCCGTGCGCTGCTATCGCCGGCGAGCCTGTTGCTGCTCGACGAGCCAA

CCTCGGCGCTGGATCCGCAGACCGCCCGGCAGGTCCTGCGCAACCTGCGCGAACGCGGCGGTGGCCG
GACCCGGGTGATCGTCGCCCATCGTCTGGCCGAAGTCAGCGATGCCGACCTGATCCTGGTGCTGGTC
GCTGGCCGTCTGGTCGAACGCGGCGAGCACGCGGCGCTGTTGGCGGCGGACGGCGCCTATGCGCGCT
TGTGGCGTGAACAGAACGGCGCGGAGGTGGCGGCATGA

The VIR17 protein (SEQ ID NO:34) encoded by SEQ ID NO:33 is presented using the one-letter amino acid code in Table 19B.

Table 19B. Encoded VIR10 protein sequence (SEQ ID NO:34)

MTPVLWRLLRTYRWRLAAAMGLQALAGLCSLLPWMLLAWLAEPLARGQAQPALLALVLLAVLAWL
GCQALAAHLAHRVDADLCNDLRLRLLAHLQRLPLDWFGRQGPDGVARLVEQDVRALHQLIAHAPN
DLSNLLVVPLVALLWLAWLHPWLLLFCLLPLVLAAAGFLLLRSARYRDLVLRRNAALERLSADYG
EFAHNLLLARQYPGAGIQQGAEASAAAFGEAFGAWVKRVGHLAALVYVQLSTPWLLAWVLLGALA
LDALGVPLALGQACAFLLLLRALAAPVQALGHGGDALLGARAAAERLQQVFDQAPLAEGRSTREP
VDGAVALHGLGHAYEGVEVLADIDLELEDGSLVALVGPSGSGKSTLLHLLARYMDAQRGELEVGG
LALKDMPDAVRHRHIALVGQQAAALEISLADNIALFRPDADLQEIRQAARDACLDERIMALPRGY
DSVPGRDLQLSGGELQRLALARALLSPASLLLLDEPTSALDPQTARQVLRNLRERGGGRTRVIVA
HRLAEVSDADLILVLVAGRLVERGEHAALLAADGAYARLWREQNGAEVAA

The role of VIR17 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT18

A *Pseudomonas* bacterial mutant (MUT18) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the putative ATP-binding component of ABC transporter, pchI (PA4222). This gene encodes the VIR18 nucleic acid (SEQ ID NO:35) shown in Table 20A.

Table 20A. VIR18 Nucleotide Sequence (SEQ ID NO:35)

ATGACCCTGTTCGAACGAATGCGTGCGCTGCCCGAAGACTGCCGTGCCGCGTTGCGCCGGGCGAGCG
CCTGGGCGGTCCTGGCGGCGCTGCTGGACGCCGCTTGCGGCGTATTGCTGGTGCCGTTGGTCGAGGC
CTGGTTCGCCGAAGGCGCGTTGCCCTGGCGCTGGGTCGCCGCGTTGCTCGGCTTGAGCCTGGCGCAG
GCGCTGTTGCAGTACCTGGCCCTGCGTCGCGGTTTCGCCGCCGGCGGCTCGCTGGCGGCTGGACTGG
TGCGCAGCCTGGTGGCGCGCTTGCCGCGCCTGGCGCCGCCGGCGCTGCGCCGGGTCGCGCCGGCCGA
AGGCCTGCTGCGCGGCCCGGTGATGCAGGCGATGGGCATTCCGGCGCACCTGCTGGGGCCGCTGATC
GCCGCGTTGGTGACGCCGCTCGGGGTGATCCTCGGGCTGTTCCTGATCGACCCGTCCATCGCCCTCG
GCCTGCTCCTTGCTGGTGCCTTCCTCGCCGCGCTGTTGCGCTGGAGCGGGCGGCGCAATCTGGCGGC
GGAGGATGCCCGGCTGGCCGCCGAGCGCGACGCCGCACGGCAGTTGCAGGCGTTCGCCGAACGCCAG
CCACTGCTGCGCGCGGCGCAGCGCGAAAGCGTCGCCCGCCAGGGGCTGGAAGAGGCCTTGCGCAGTC
TCCACCGCAGCACCCTGGATCTGTTGCGGCGCAGCCTGCCCAGCGGCCTCGGCTTCGCCCTGGCGGT
GCAGGCGGCGTTCGCCTTCGCCCTGCTCGGCGGCGCCTGGGCGGTGGAGCGGCAATGGCTGGACGGC
GCTCGGCTGGTGGCCGTGCTGGTGCTGCTGGTGCGCTTCATCGAGCCGCTGGCCCAGCTCACCCATC

TCGACCAGGCGTTGCGCGGCGCCTGGCAGGCGCTGGATACCCTGCTGCGGGTTTTCGCCCTGGCTCC
GCTGCGCAGCCCCGAGCCGGGCGAGCGGCCGCACGACGCCAGCCTGGCGGCCGAGGCCGTGGAATTG
CGCCTGGAAGATGGCCGCGCCTTGCTCGAGGACATTTCCCTGAGGCTGGAGCCGGGTTCGCTGAACG
TCCTCGTCGGACCCTCCGGGGCCGGCAAGAGCAGCCTGCTGGCGCTGCTCGGGCGGCTCTACGACGT
CGATGCCGGGCGTGTCCTGCTGGGTGGCGTGGATATCCGCCGGTTGAGCGAAACGACCCTCGCCGCC
AGTCGTAACCTGGTGTTCCAGGACAACGGCCTGTTCCGCGGCAGCGTTGCCTGGAACCTGCGCATGG
CGCGAGCGGACGCCGATCTCGAAGCGCTGCGCGAGGCGGCGCGGGCGGTTGGCCTGCTGGAAGAGAT
CGAGGCCTGGCCGCAGGGCTGGGACAGCGACGTCGGTCCCGGCGGCGCGCTGCTGTCCGGCGGCCAG
CGGCAACGCCTGTGCCTGGCTCGCGGGCTGCTCTCGACGGCGCCGTTGCTGCTGCTCGACGAGCCCA
CCGCCAGCCTCGACGCCGCCAGCGAGGCGCAGGTGCTGCGCAGCCTGCTCGGGTTGCGCGGCCGGCG
CACCCTGCTGGTAGTGACCCACCGCCCGGCGCTGGCGCGTCAGGCCGACCAGGTACTGCTGCTGGAG
GAGGGGCGCCTGCGCCTCAGCGGACTTCACGCCGATCTGCTCGTCCGGGACGACTGGTATGCCGGTT
TCGTCGGGCTGGCGGGCGAGGAAAGTTCCGCGACGGTCGTGGATCGATAG

The VIR18 protein (SEQ ID NO:36) encoded by SEQ ID NO:37 is presented using the one-letter amino acid code in Table 20B.

Table 20B. Encoded VIR18 protein sequence (SEQ ID NO:36)

MTLFERMRALPEDCRAALRRASAWAVLAALLDAACGVLLVPLVEAWFAEGALPWRWVAALLGLSL
AQALLQYLALRRGFAAGGSLAAGLVRSLVARLPRLAPPALRRVAPAEGLLRGPVMQAMGIPAHLL
GPLIAALVTPLGVILGLFLIDPSIALGLLLAGAFLAALLRWSGRRNLAAEDARLAAERDAARQLQ
AFAERQPLLRAAQRESVARQGLEEALRSLHRSTLDLLRRSLPSGLGFALAVQAAFAFALLGGAWA
VERQWLDGARLVAVLVLLVRFIEPLAQLTHLDQALRGAWQALDTLLRVFALAPLRSPEPGERPHD
ASLAAEAVELRLEDGRALLEDISLRLEPGSLNVLVGPSGAGKSSLLALLGRLYDVDAGRVLLGGV
DIRRLSETTLAASRNLVFQDNGLFRGSVAWNLRMARADADLEALREAARAVGLLEEIEAWPQGWD
SDVGPGGALLSGGQRQRLCLARGLLSTAPLLLLDEPTASLDAASEAQVLRSLLGLRGRRTLLVVT
HRPALARQADQVLLLEEGRLRLSGLHADLLVRDDWYAGFVGLAGEESSATVVDR

The role of VIR18 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT19

A *Pseudomonas* bacterial mutant (MUT19) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as a gene cluster encoding the *P. aeruginosa* serotype 09 putative O-antigen biosynthesis pathway (VIR19). The insertion site nucleic acid sequence identifying the VIR19 gene in MUT19 is shown in Table 21.

Table 21. MUT19 Transposon Insertion Site (SEQ ID NO:37)

CTCTTTCAGCCGCACGCGGCGCACCTCGTGTGTGATCAGTGAGTGGTTTGCAACTGCGGGTCAAG
GATCTGGATTTCCCTCACANGTNCGATCATCGTGCGGGAGGGCAAGGGCTCCAAGGATCGGGCCT
TGATGTTACCCGAGAGCTTGGCACCCAGCCTGCGCGAGCAGGGNNAATTGATCCGGTGGATGACC

TTTTGAATGACCTTTAATAGATTATATTACTAATTAATTGGGGACCCTANAGGTCCCCTTTTTTA
TTTTAAAAATTTTTTCACAAAACGGTTTATTTNCATAAAGCTTGCTCAATCAATCACCNTATCCN
CGGGAATTCGGCCTAGGCGGCCAGATCTGATCAAGAGACAGACCTCCAGCTTTGCATCCGGAGCG
ACCACACGAGCGAGGTCAGTCACTTTCATCGAAGGAATTTTCTTGACATAGATCTCACCACCTTC
CATGTCCTCAAAGGCATGCCACACTAACTCGACGCCCTCCTCCAAAGAAATCATGAACCGGGTCA
TCCGCTCATCAGTGATAGGCAAGACGCCCTTGTCCTTG

The role of this cluster in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

5

B. Attenuated *Klebsiella* Mutants

MUT20

A *Klebsiella* bacterial mutant (MUT20) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
10 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding a hypothetical transcriptional regulator in met G-dld intergenic region (VIR20). The insertion site nucleic acid sequence identifying the VIR20 gene in MUT20 is shown in Table 22.

15

Table 22. MUT20 Transposon Insertion Site (SEQ ID NO:38)

ACGCAGGATATCTTCTTCATCAAATTGTCGATGCCCGCCTTCGCTACGCTGCGGTTTCAGTAGACCG
TAACGACGCTGCCAGGCGCGCAGTGTGACCGGATTGATTCCGCAACGTTCGGCGACTTCACCGATAC
TGTAAAACGCCATAGCAGCCTCACATCAACCTGATACCTTAATACCTAAACTAACGAATTCAGGCAT
CCTGTACAACTCTATTTTCTTGTACAGATAAAGATATCAGGTTGCGGCTCACAGCGCCCGGGAAAAA
AGATGAAAAAATGTTTAGCTGATTTCGCGGTGGTTCATTTTTTCTCCGGCCATGCGACGGCGGGTAG
GCCCCCCAGGCGCGCGCTGGCGAACAAATTGCCCTGAAACTGTGAAATACCGGCTGATTCCAGCCAC
ATCCACTCTTCAGCACGCTCAACGCCGACGGCTGAGACCGCAATCTCCAGAGAAGTACAGCATTTGA
TAATCGCCTG

MUT21

A *Klebsiella* bacterial mutant (MUT21) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
20 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding •-cystathionase (VIR21). The insertion site nucleic acid sequence identifying the VIR21 gene in MUT21 is shown in Table 23.

Table 23. MUT21 Transposon Insertion Site (SEQ ID NO:39)
GACCATGTGCTGATGACCAATACCGCCTATGAGCCAAGCCAGGACTTTTGTACCAAAATTCTCGCCA AACTCGGCGTCACCACCAGCTGGTTCGATCCCTTAATCGGCGCCGATATCGCCCGTCTGGTTCGCCC TGAGACCCGCGTGGTGTTCCTCGAATCGCCCGGCTCGATCACCATGGAAGTGCACGATGTGCCGGCG ATAGTCGCCGCCGTGCGTCAGGTCGCCCCGGAAGCGATTATCATGATCGATAACACCTGGGCGGCGG GGATCCTGTTTAAAGCCCTGGATTTTGGCATTGATATTTCCATTCAGGCAGGCACCAAATACCTGAT CGGCCATTCCGACGCCATGGTGGGCACCGCGGTGGCGAACGCGCGCTGCTGGCCGCAGCTGCGTGAA AATGCCTACCTGATGGGGCAAATGCTGGACGCCGATACTGCCTATATGACCAGCCGCGGCCTGCGAA CCCTGGGCGTGCGCCTGCGTCAGCATCATGAAAGCAGCCTGCGCATC

MUT22

A *Klebsiella* bacterial mutant (MUT22) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as ribosome binding factor A (VIR22). The insertion site nucleic acid sequence identifying the VIR22 gene in MUT22 is shown in Table 24.

Table 24. MUT22 Transposon Insertion Site (SEQ ID NO:40)
CTTTTGGCCCCTTTTTTGTCTTTATTCTGGAGAACTTATTATGGCGAAAGAATTTGGTCGCCCGCAG CGTGTGGCCCAGGAGATGCAAAAAGAGATTGCCATCATCCTGCAGCGTGAAATTAAAGATCCGCGTC TGGGCATGATGACCACCGTTTCCGGTGTGGAAATGTCCCGTGACCTGGCCTATGCCAAGGTGTATGT CACCTTCCTTAACGACAAAGATGAAGCCGCGGTGAAAGCGGGCATCAAAGCGCTGCAGGAAGCTTCT GGCTTTATCCGCTCTCTGCTGGGGAAAGCGATGCGTCTGCGCATCGTACCGGAACTGACTTTCTTCT ACGACAACTCACTGGTGGAAGGGATGCGTATGTCCAACCTGG

MUT23

A *Klebsiella* bacterial mutant (MUT23) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding aspartokinase/homoserine dehydrogenase (VIR23). The insertion site nucleic acid sequence identifying the VIR23 gene in MUT23 is shown in Table 25.

Table 25. MUT23 Transposon Insertion Site (SEQ ID NO:41)
GCCCAGCCCGCTTTCCCGCTTGCCCAGTTAAAAGCCTTCGTGGAGCAGGAATTTGCTCAGATTAAGC ATGTTCTGCACGGCATCAGCCTGCTGGGTCAGTGCCCGGACAGCGTCAATGCCGCGCTGATCTGCCG CGGCGAAAAGCTCTCCATCGCCATCATGGCGGGTCTGCTGGAAGCCCGTGGACACAAAGTCAGTGTC ATTAACCCGGTCGAAAAACTGCTCGCCGTGGGTCACTATCTGGAATCCACCGTCGATATCGCCGAAT

CCACCCGCCGCATTGCCGCCAGCCAGATCCCGGCAGACCATATGATCCTGATGGCCGGGTTTACCGC
CGGCAATGAGAAAGGCGAGCTGGTGGTGCTGGGGCGTAACGGCTCCGACTACTCGGCTGCGGTACTG
GCCGCCTGCCTGCGCGCTGACTGCTGCGAAATCTGGACCGATGTCGACGGAGTGTACACCTGCGATC
CGCGTCAGGTGCCGGATGCGCGCCTGCTGAAATCGATGTCTTATCAGGAGGCGATGGAGCTCTCCTA
CTTTGGCGCGAAAGTGCTGCACCCGCGCACCATTGCCCCTATCGCCCAGTTCCAAATCCCATGCCTG
ATTAAAAATACCGGCAACCCCC

MUT24

A *Klebsiella* bacterial mutant (MUT24) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding cystathione • -synthetase (VIR24). The insertion site nucleic acid sequence identifying the VIR24 gene in MUT24 is shown in Table 26.

Table 26. MUT24 Transposon Insertion Site (SEQ ID NO:42)

GGCGCAGCGTCTGCTCGTCACCGTCAAGCTCGAAGCTTAACATTGCGCCAAAACCTTTTTGCTGACG
CGCCGCAATTTCATGCCCCTGGTTTTCCGGCAGCGATGGATGATACAGCTTTTTCACCAGCGGCTGG
GTTTTCAGATACTCAACGATCGCCAGGGCATTTCGCTGCGCCACTTCCATCCGTGGAGACAGCGTCC
GCAGCCCGCGCAACAGCAGATAGCTGTCGAAGGCGCTGCCGGTGACGCCAATATTATTCGCCCACCA
TGCCAGTTCGGTGACAGTTGCCGGATCTTTGGCAATCACCACCCCGGCCACCACATCGGAGTGACCA
TTGAGGTATTTGGTACAGGA

MUT25

A *Klebsiella* bacterial mutant (MUT25) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding phosphoribosylformylglycinamidine synthase (VIR25). The insertion site nucleic acid sequence identifying the VIR25 gene in MUT25 is shown in Table 27.

Table 27. MUT25 Transposon Insertion Site (SEQ ID NO:43)

GTTGCGTCCCAGGCGGGTAAACGCATCCTGCAGGTAGTCAATTTCGTCGTCGGCCAGCGCCAGACCC
AGACGGAGGTTGGCGTCAATCAGCGCCTGACGCCCTTCGCCCAGCAGGTCGACGCTGGTGACCGGCG
TCGGCTGATGGTGAGCGAACAGCTTCTCGCCCGCTTCCAGCTCGTCGAAGACGCTCTCCATCATGCG
GTCATGCAGCTCCGCCGCCACCGCGGCCCACTGCGCTTCGGTCAGGGTTGAGGCTTCAACGTAATAC
GCCACGCCGCGCTCAAGACGCACAACCTGCGCCAGACCGCAGTTGTGAGCGATATCGGTAGCTTTAG
AAGACCAGGGAGAGATGGTGCCAGGGCGAGGGGTCACGAGCAGTAATTTACCGGTCGGGGTATGGCT
GCTTAAGCTCGGGCCATACTGAAGCAGTCGCGCCAGGCGCTCGCGATCGTCAGCGCTCAGCGGGGCG
TTCAGATCGGCAAAATGAATATATTCGGCAT

MUT26

A *Klebsiella* bacterial mutant (MUT26) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding homoserine transsuccinylase (VIR26). The insertion site nucleic acid sequence identifying the VIR26 gene in MUT26 is shown in Table 28.

Table 28. MUT26 Transposon Insertion Site (SEQ ID NO:44)

GTATTGGCATCGTACTCCTGGGCTGGCCGGTGACAAAGGCGATGCGCTTATCTTTGCTGGCGAACAA
ATACGCATCGCCCTCTTCCGTCTCCGCGAGGATCTCGAGATCGGTATAGTCGCGAATAAGTCCGGCC
GGAAAATCAGCATAGCGTGAGTGCGGGGCCAGGAAAGAGTCGTCGAAACCGCGGGTCAGTAAGGCGT
GCGGATGAAGAATATGGTGTTCATAGACGCCGGAAATCTTTTCGGCGCGGGTCTGCTTGGGAATGCC
GTACAGAATGTTCAGCGCGGCCTGAACCGCCCAACAGACGAACAGCGTCGAAGTGACGTGATCCTTG
GCCCACTCCAGCACCTGTTTGATCTGCGGCCAGTAAGCAACATCGTTAAACTCAACCAGGCCTAAAG
GAGCGCCGGTAACAATCAGGCCGTCAAAGTTCTGATC

MUT27

A *Klebsiella* bacterial mutant (MUT27) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 3'-phosphoadenosine 5'-phosphosulfate reductase (VIR27). The insertion site nucleic acid sequence identifying the VIR27 gene in MUT27 is shown in Table 29.

Table 29. MUT27 Transposon Insertion Site (SEQ ID NO:45)

GAGGTTCATATGTCCGTACTCGATCTAAACGCGCTTAATGCATTGCCGAAAGTGGAACGCATTCTGG
CACTCGCGGAAACCAACGCCCAACTGGAAAAGCTTGACGCCGAAGGGCGTGTGGCGTGGGCGCTGGA
AAATCTGCCGGGAAACTATGTGCTGTCGTCGAGCTTTGGCATTCAGGCGGCGGTAAGTTTGCATCTG
GTGAATCAGATCCGCCCGGACATTCCGGTGATCCTCACCGATACCGGCTACCTGTTCCCGGAAACCT
ATCAGTTTATTGACGAGCTGACGGACAAG

MUT28

A *Klebsiella* bacterial mutant (MUT28) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the

gene encoding Sfi protein (VIR28). The insertion site nucleic acid sequence identifying the VIR28 gene in MUT28 is shown in Table 30.

Table 30. MUT28 Transposon Insertion Site (SEQ ID NO:46)

TGTTAAAGCGTGCGTTCTACAGCCTGTTAGTCCTGCTCGGCCTGCTGCTGTTGACCGTGCTGGGCCT
TGACCGCTGGATGAGCTGGAAAACCGCGCCCTATATCTATGATGAACTGCAGGACCTGCCCTACCGT
CAGGTCGGTGTGGTGCTGGGCACCGCCAAATATTACCGCACCGGCGTCATCAATCAGTATTACCGTT
ACCGCATCCAGGGTGCGCTGAACGCCTACAACAGCGGCAAGGTCAACTATCTCCTGCTGAGCGGCGA
TAATGCTCTGCAAAGCTACAATGAACCGATGACCATGCGTCGGGACCTGATTAAAGGCGGCGTCGAT
CCCGCGGATATCGTACTGGACTATGCCGGTTTCCGTACCCTCGACTCGATCGTCCGTACCCGGAAAG
TGTTCGACACCAACGACTTCATTATCATCACCCAGCGCTTCCACTGCGAACGGGCGCTGTTTATCGC
CCTGCATATGGGGATCCAGGCCCAGTGCTACGC

MUT29

A *Klebsiella* bacterial mutant (MUT29) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding transcriptional activator protein LysR (VIR29). The insertion site nucleic acid sequence identifying the VIR29 gene in MUT29 is shown in Table 31.

Table 31. MUT29 Transposon Insertion Site (SEQ ID NO:47)

CGCTGAACCTCCTCAAACAAACGCAGGCCCTGCACCTGTCGGCTGCAGGCGACCAGCGTGGATCCGC
TCAAACAGCTGCAGGCCGAGCACCTTCTCAAAGCGCGCCAGCTCGCGGCTGACCGTGGGTTGCGAGG
TGTGCAGCATCCGCGCCGCTTCGGTCAGGTTGCCGGTGGTCATCACCGCGTGAAAGATTTCGATATG
ACGCAAATTGACGGCTGGCATGCGGTCTCCGTGAGGCTCGGCTGGAACCATATCATTTTTGCATAGA
GTCGCGATAAAACGATATTTTTTATTCGTCTGTCACTGTGGCGTAATCAGAAAAAACAGCGACCAAC
ACACGCACTGCACCGGAGTTCTTATGCCACACTCGCTTTACGCCACCGATACTGACCTGACCGCGGA
CAACCTGCTGCGCCTGCCGGCGGAATTTGGCTGCCCGGTCTGGGTCTATGATGCGCAGATTATTCGC
CGCCAGATAGCCCAGCTCAGCCAGTTTCGAC

MUT30

A *Klebsiella* bacterial mutant (MUT30) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding TrpD (VIR30). The insertion site nucleic acid sequence identifying the VIR30 gene in MUT30 is shown in Table 32.

Table 32. MUT30 Transposon Insertion Site (SEQ ID NO:48)
GGCTTCCACCCAAATCGCTTTGTCGGCAACGATTTTTGCTAAAACGGCTTTGCATTCTTTACCCTCT TGCCCGCTAAGTGCGGTCACTCTGTCATAGGCCGCGCCGCTGCTGCAGCACATCCAGTACCTGCTGA GCGTTAGCTTTCAGATCTTCATGCCCGTGTAAACGCATCAATATGGCGACGTTGGCGGCGACGGCGG CTTCGTGAGCGGCTTCACCTTTACCTTG

MUT31

A *Klebsiella* bacterial mutant (MUT31) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding N-acetylglucosamine-6-phosphate deacetylase (VIR31). The insertion site nucleic acid sequence identifying the VIR31 gene in MUT31 is shown in Table 33.

Table 33. MUT31 Transposon Insertion Site (SEQ ID NO:49)
TGGCTCAACGCTGCTCAGTGGTGCGAGGTGTCACTTTGGTGATCACATCGGCGTTGTCTGCACAGTG AAATCAGATCCAGCGCCGCGTCCGGTTTTACGCACGTAGTCCGGATTGTGGGTGCCTTTCTTAACGA TATTCAGCCACGGCCCTTCGAGATGCAGGCCCAGCGCCTGGTTCGGATGTTTTTGCAGATATTCGCG CATCACGCGCACGCCTTGCTTCATCAGATCGTCGCTGGAGGTAATCAGCGTCGGCAGGAAGCTGGTG CAGCCTGAGCGTTCGTTGGCCTTCTGCATGATCTCCAGCGTTTCGACAGTGACCGCCTCTGGGCTGT CGTTAAACTGCACGCCGCCGCAGCCGTTGAGCTGGACGTCGATAAAACCGGGGGCGATTATTGCGCC GTTGACTGAGCGCTGCTCGATGTCAGACGGCAAATCTGCCAGCGGACAAAGACGTTCGATAAAG

MUT32

A *Klebsiella* bacterial mutant (MUT32) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encodingWaaQ (VIR32; Regué *et al.* J. Bacteriol. 183(12): 3564-73, 2001). The insertion site nucleic acid sequence identifying the VIR32 gene in MUT32 is shown in Table 34.

Table 34. MUT32 Transposon Insertion Site (SEQ ID NO:50)
TTAAGCACCATATCGTACCGCTGCTGGCGCAGCGTCTGAATGAGCTGCCATTGCATCTTCAGCTGAT ACCTTTTTCCCTGGCTTTTTCCAGCGGCGATCGAGACCATAAATATGGTGGATATCGGGGTTGGCTG CGAGCATATCCCGGGTCTCTTCATACAACAGGACATCCACGCTGGCGGCGGGGTACTGCTGTTTCAG CGCGTGAATAAGCGGCGTGATCAGCAGCATGTCGCCATGATGGCGCAGCTTAATGACCAGGATCCGC GCCGGGTTCAACGGGCCGCGGGAGAGGGTTTCAGGCGTCATACTCTGTTCTTCATCCAGGATAAGGG TTCCGATTCTAGGGGATCAGACAGATTGAGAGAAGCGTTGTATTGCTCTACCATGACCCGATACGTA TGGCCTGAGGACGTTTTCGTGCACAATCCCGCAATTTCTCATCACGAT

MUT33

A *Klebsiella* bacterial mutant (MUT33) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 2-isopropylmalate synthase (VIR33). The insertion site nucleic acid sequence identifying the VIR33 gene in MUT33 is shown in Table 35.

Table 35. MUT33 Transposon Insertion Site (SEQ ID NO:51)

CACTCAGGCTTGCCTGTAACGCTTGTTCGCCATCACGTAAGGTCGTATCGAAAATAATGACTTGCTG
GCTCATGGTTTGGATCCTTAGTCTGTGTCCTGGCGCCTTGTTGACGAGCATAAAAAAACCCGCGCCA
AGGCGCGGGTTTTATAGTCTTGCTGGAAGATGACTTAACGCTGAACGTCGCCCAACAGCCTACCGAG
CAAATGGCATGCGTTTAGTAGTAGTAGGCTGGTGATACGAGCGGTGCGAATCATTGCGTCAAACTCC
AGATGAAATCGTTATGCTTTTAGAGTTACTGGATAGCCGTTTTAAAGTCAACCCCTGGCATGGAAAA
AGCGTTTTGGGCTGACTAAATGAATTAGCAAAATGTGCTGATGTAAGCCCCATTTTGCCGAAGATCC
TATTTTGGACCGAAGGCGGTTTATCCCCAATTTGTTTCATTTGAAAAA

MUT34

A *Klebsiella* bacterial mutant (MUT34) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding histidinol dehydrogenase (VIR34). The insertion site nucleic acid sequence identifying the VIR34 gene in MUT34 is shown in Table 36.

Table 36. MUT34 Transposon Insertion Site (SEQ ID NO:52)

CGCTGAACCGCTATCCGGAGCCGCAGCCGAAGTGCCGTGATTGAGAGCTACGCCCGCTACGCCGAGG
TCAAACCGGAGCAGGTGCTGGTCAGCCGCGGCGCCGACGAAGGCATCGAGCTGCTGATCCGCGCCTT
CTGTGAGCCCGGCGAAGACGCGGTGCTCTACTGCCCGCCGACCTACGGCATGTACAGCGTCAGCGCC
GAGACCATCGGCGTCGAGTGCCGCACCGTGCCGACGCTGGCCAGCTGGCAGCTCGACCTGCCGGGCA
TCGAAGCGCGGCTGGACGGCGTGAAGGTGGTGTTTGTCTGCAGCCCGAACAACCCGACCGGGCAGAT
TATCGACCCGCAGTCGATGCGCGACCTGCTGGAGATGACCCGCGGCAAAGCCATCGTGGTGGCCGAC
GAAGCCTATATTGAATTCTGCCCGCAGGCGACGCTCGCCGGCTGGCTCAGCGACTATCCGCACCTGG
TGGTGCTGCGCACGCTGTCCAAAGCCTTCGCCCTCGCCGGCCTGCGCTGCGGCTTCACCCTCGCCAA
CGCCGAGGTGATTAACGTGCTGCTGAAAGTGATCGCCCC

MUT35

A *Klebsiella* bacterial mutant (MUT35) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding UDP-galactopyranose mutase (VIR35; Clarke *et al.*, J. Bacteriol., 177: 5411-18, 1995). The insertion site nucleic acid sequence identifying the VIR35 gene in MUT35 is shown in Table 37.

Table 37. MUT35 Transposon Insertion Site (SEQ ID NO:53)

CGTATATTTCATCGTACAGAAACCGTAAACACAGGCATTGGCTGATTTTCAGTGAGTGAATTTAAAT
AGACTTCTGCCGTTTTCAATGCTTCGGCGATGGTCACATCCATATCAAGGTAACGGTAGGTTCCAAG
ACGACCGACAAAAGTGATGTTGGTTTCATTCTCGGCCAATGACAAATATTTTTCAAGAAGAGCCATT
TCTCCCATCTGGCGAATAGGATAGTAAGGAATATCATTTTCTTCACAAGCACGGCTATACTCTTTAT
AACAAACAGAGCCGTCGTGTTGTTCCCAGGGAGAAAAATATTTATGTTCAGTGATGCGAGTATAGGG
CACATCCACAGAACAGTAGTTCATCACTGCGCATCCCTGG

MUT36

A *Klebsiella* bacterial mutant (MUT36) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding O-antigen export system permease protein rfba (VIR36; Bronner *et al.*, Mol. Microbiol., 14: 505-19, 1994). The insertion site nucleic acid sequence identifying the VIR36 gene in MUT36 is shown in Table 38.

Table 38. MUT36 Transposon Insertion Site (SEQ ID NO:54)

GTACGCCGATTTTATATGCGTCTGATATGATTCCGGAAAAATTTAGCTGGATAATTACCTACAATCC
GCTAGCGAGTATGATTCTTAGTTGGCGTGATTTATTCATGAATGGGACTCTTAATTTTGAGTATATT
TCTATACTCTATTTTACGGGAATTATTTTGACGGTTGTCGGTTTGTCTATTTTCAATAAATTAAAAT
ATCGATTTGCAGAGATCTAAAAGTGCGCTATAAGAGCAGCATGCTAGGCTATTTATGGTCAGTAGCA
AATCCATTGCTTTTTGCCATGATTTACTATTTTATATTTAAGCTGGTAATGAGAGTACAAATTCCAA
ATTATACAGTTTTCCTCATTACCGGCTTGTTTCCGTGGCAATGGTTTGCCAGTTCGGCCACTAAC

MUT37

A *Klebsiella* bacterial mutant (MUT37) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated

microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding uridyltransferase (VIR37). The insertion site nucleic acid sequence identifying the VIR37 gene in MUT37 is shown in Table 39.

Table 39. MUT37 Transposon Insertion Site (SEQ ID NO:55)

CGAGCCACCCACTGTAGCGTATGGATATCGCGCAAGCCGCCGGGGCTGCTTTTCACGTCCGGCTCGA
GGTTATAGCTGGTGCCATGATAGCGCTGATGACGGACGTTCTGCTCTTCGACCTTGGCGGCGAAGAA
CTTTTCCGATGGCCAGAAGCCGTCGCTAAAAATATGTTTTTGCAGTTCAAGGAACAGCGCGACGTCG
CCGATCAGCAGGCGCGATTCGATTAAGTTGGTGGCAACGGTCAGATCCGAGAGACCTTCCAGCAGGC
ACTCTTCGAGGGTGCGTACGCTGTGGCCCACCTCCAGCTTGACGTCCCACAGCAGGGTGAGCAGTTC
GCCGACTTTTTGCGCCTGGTCGTCCGGCAGTTTTTTACGACTGAGGATCAGCAGATCGACGTCTGAG
AGCGGGTGCAG

MUT38

A *Klebsiella* bacterial mutant (MUT38) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyridoxine phosphate biosynthetic protein PdxJ-PdxA (VIR38). The insertion site nucleic acid sequence identifying the VIR38 gene in MUT38 is shown in Table 40.

Table 40. MUT38 Transposon Insertion Site (SEQ ID NO:56)

CTTAACCCGCACGCTGGCGAAGGCGGCCATATGGGAACAGAAGAGATAGACACCATCATTCCGGTGC
TGGAAGAGATGCGCGCAAAGGGGATGAACCTCAGCGGTCCGCTGCCGGCAGACACTCTCTTTCAGCC
GAAATATCTTGATCATGCCGATGCGGTACTCGCGATGTACCACGATCAGGGCCTGCCCGTGCTAAAA
TACCAGGGCTTTGGCCGCGGCGTGAACATTACGCTCGGTTTACCTTTTATTCGTACCTCCGTCGACC
ACGGCACCGCACTGGAATTAGCGGGCCAGGGAAAAGCGGACGTCGGCAGTTTTATCACGGCGCTTAA
TCTCGCCATCAAAATGATTGTTAATACCCAATGAATAATCGAGTCCATCAGGGCCATTTAGCCCGCA
AACGCTTCGGGCAGAACTTCCTCAACGATCAGTTTGTGATCGACAGCATCGTCTCGGCGATTAACCC
GCAGAAAGGCCAGGCGATGGTTGAAATCGGC

MUT39

A *Klebsiella* bacterial mutant (MUT39) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding triose phosphate isomerase (VIR39). The insertion site nucleic acid sequence identifying the VIR39 gene in MUT39 is shown in Table 41.

Table 41. MUT39 Transposon Insertion Site (SEQ ID NO:57)

GGGTCTGACCCCGGTTCTGTGCATCGGTGAAACCGAAGCCGAAAACGAAGCGGGCAAAACGGAAGAA
GTTTGCGCACGTCAGATCGACGCCGTGCTGAAAACCCAGGGCGCTGCCGCTTTCGAAGGCGTGGTTA
TCGCTTACGAACCAGTATGGGCTATCGGTACCGGCAAATCAGCGACCCCGGCTCAGGCGCAGGCGGT
GCACAAATTCATCCGTGACCACATTGCTAAAGCTGACGCCAAAATCGCTGAGCAAGTGATCATCCAG
TACGGCGGTTCCGTTAACGCTGGCAACGCCGCAGAGCTGTTCACCCAGCCGGACATCGACGGCGCGC
TGGTTGGCGGCGCCTCCCTGAAAGCTGACGCTTTCGCGGTGATCGTTAAAGCAGCAGAAGCAGCGAA
AAAAGCGTAATTCGCTTTTCCCGGTGGCGACACGCGACCGGGTTGACTGACAAAACGTGGGAGCCCG
GCCT

MUT40

A *Klebsiella* bacterial mutant (MUT40) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding aldehyde dehydrogenase (VIR40). The insertion site nucleic acid sequence identifying the VIR40 gene in MUT40 is shown in Table 42.

Table 42. MUT40 Transposon Insertion Site (SEQ ID NO:58)

GGTGGCGCACCCTGGCGTCGTTTGTGTAGAAATTATGAATATTAATACCAGGAAAATTCCTAATTTT
TGTGTACGCTCTGACGAGCGCACAATAAAACAAGACGAATTTTTGAACAATTGTCTTTAAATTTGTT
AATTGAATTGATCTGTTGTTGTTTAAAGGTATTTGAATTTCTTTTGTATAGATATGTAAATTAACAT
TGAAAAGCCATTTCAAAAATTAAATATATGGCGAACATAGCTATTAACTTATAGTTAACATCTTCCC
GGGTTGCCTTTTGATACTTCGGGTAATATATTTATTTCGCACATCAAAATAACTCTTTTTTCTTCTG
TTTGTTATTCATGGCCATCTATTGGCGAAATAAGGCAGAGTAGAGGGGGATGTGCCTAATATCCTGC
GGAAGGAACGCAATGTACATTTACAGGGAGGAGCTGACGAGCCGTTTCGCGATAGCTTTAG

MUT41

A *Klebsiella* bacterial mutant (MUT41) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding galacosyl transferase (VIR41; Clarke *et al.*, J. Bacteriol., 177 : 5411-18, 1995). The insertion site nucleic acid sequence identifying the VIR41 gene in MUT41 is shown in Table 43.

Table 43. MUT41 Transposon Insertion Site (SEQ ID NO:59)

TTGGTGGTGTGCTCGCGAAGAAATTTAATCTGCCGGTCATCGTAAGTTTTGTTGGGCTTGGAAGAGT

ATTTTCTTCTGACAGCATGCCTTTAAAATTATTGCGGCAGTTTACTATTGCTGCATATAAATATATT
GCCAGTAATAAGCGCTGTATATTTATGTTTGAACATGACCGCGACAGAAAAAAACTGGCTAAGTTGG
TTGGACTCGAAGAACAACAGACTATTGTTATTGATGGTGCAGGCATTAATCCAGAGATATACAAATA
TTCTCTTGAACAGGATCACGATGTCCCTGTTGTATTGTTTGCCAGCCGTATGTTGTGGAGTAAAGGA
CTGGGCGACTTAATTGAAGCGAAGAAAATATTACGCAGTAAGAATATTCACTTTACTTTGAATGTTG
CTGGAATTCTGGTCGAAAATGATAAAGATGCAATTTCCCTTCAGGGTCATTGAAAATTGGCATCAGC
AAGGATTAATTAACTGGTTAGGTCGTTCGAATAATGTTTGCGATCTTATTGAGCAAT

MUT42

A *Klebsiella* bacterial mutant (MUT42) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding siroheme synthetase (VIR42; Kolko *et al.*, J. Bacteriol., 183 : 328-35, 2001). The insertion site nucleic acid sequence identifying the VIR42 gene in MUT42 is shown in Table 44.

Table 44. MUT42 Transposon Insertion Site (SEQ ID NO:60)

TTACTTGCCCCTTTTTGCCGAACTGAAACAAAGGCCCGTGCTGGTGATCGGCGGCGGCGAGATTGCT
GAACGTAAGATCAAGTTCCTGCTGCGCGCCCAGGCGCAGGTGCAGGTGGTCGCTGAAACGCTGTCAC
CGGCGCTGGCCGATCTGGCTGCGCGCCAGGCACTCAGCTGGCGGGCGACGGCATTCAGCGACTCGCT
GGTGGATGATGTCTTTCTGGTGATTGCGGCCACCGAGGATGAGGCGCTTAACCAGCGGGTGTTTGCG
GCAGCTAACGCGCGCTACCGGTTGGTCAACGTGGTGGATAACCAGGCGCTGTGCTCGTTTGTTTTCC
CTTCTATCGTCGACCGTTCGCCGCTGCTGGTGGCGATCTCCTCCAGCGGTAAAGCGCCGGTGTTGTC
GCGCATTCTGCGTGAAAAAATCGAAGCGCTGCTGCCGACGAATCTCGGTCGGCTGGCGGAATCAGCA
AGCT

MUT43

A *Klebsiella* bacterial mutant (MUT43) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (VIR43). The insertion site nucleic acid sequence identifying the VIR43 gene in MUT43 is shown in Table 45.

Table 45. MUT43 Transposon Insertion Site (SEQ ID NO:61)

AGCAGGGCAATGGTGGTCGGTTTCATAACATTTCCTGATGATGAAAGTCATATTAACCGGCATTCTA
ACAGCAGCATTCAGAGGGGCAATGATTTTGGGCAACCGATTACGACGATCGCCGCAAATGCTAAAAA
AGGGAGAGGGGATTACCAGCTGGCGGGCTTTTCCGCGCCGAGATTATCCAGCACGGCGCGCAGCGCC
AGGCCGTCAGGAAAGTGAAGGTCCGGGGCGATCTCGAACAGCGGCCAGAGCATAAAGCCGCGGTTTT

TCATATCGTAGTGCGGAACGGTCAGGCGCTCGCTGTTAATGACAGCATCGCCAAACAGCATGATATC
GAGGTCCAGCGTGCGCGGCCCCCAGCGTTCGGCTTTGCGCACTCGCCCCTGCTGCAGTTCGATGCGC
TGAGTATGATCGAGCAGCGTCTCGGGGGGCAGGGCGGTTTCCAGCGCAA

MUT44

A *Klebsiella* bacterial mutant (MUT44) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding glucose-6-phosphate isomerase (VIR44). The insertion site nucleic acid sequence identifying the VIR44 gene in MUT44 is shown in Table 46.

Table 46. MUT44 Transposon Insertion Site (SEQ ID NO:62)

GGCTTAACGCCAGCTATGTCAACGCTGCGGTTATGCGGATTTTTCATGCCTCTGCGGCTAACAGAAA
AAAGCCTTATGATAGCTATACTAATGGGGCTTTTTACTCCGTTTTGACCCGATTCCTGACCGGCGTC
AGGGTCAAGTCACAAAAATCATCACAATTTTCCGTCACCGGCGCTACAATCGACCGAAGTCACAATC
TCAAATCAGAAGAGTATTGCTAATGAAAAACATCAACCCAACGCAGACCTCTGCCTGGCAGGCATTA
CAGAAACACTTCGACGAAATGAAAGATGTCACTATCAGCGAGCTTTTCGCCAAAGATAGCGACCGTT
TTTCTAAATTTTCCGCGACGTTCGACGATCTGATGCTGGTGGACTTCTCCAAAAACCGCATCACTGA
AGAGACGCTGGCTAAACTGCAGGATCTGGCGAAAGAGACTGACCTGGCGGGCGCTATCAAGTCGATG
TTCTCAGGTGAGAAGATCAACCGCACCGAAGACCGCGCGGTACTGCACGTCGCGCT

MUT45

A *Klebsiella* bacterial mutant (MUT45) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding DNA methylase (VIR45). The insertion site nucleic acid sequence identifying the VIR45 gene in MUT45 is shown in Table 47.

Table 47. MUT45 Transposon Insertion Site (SEQ ID NO:63)

TGCTTCATCCGCATCTCCTTGAAATTTATTTGGTCTTAGGCGGACGGTAGAGCGCTAATAGCTCGTC
CACCTTTTTACGCGTACCACCGTTGCTGCTGATGCTGCGCCGCACCTTCACAATATGCGTTTCTGCC
GCGTTTTTATACCATTCCTGCGTCAGCGGCGTGCGGTGGTTGGAAATCAGCACCGGGATGCGCTTTT
TCATCAGCGATTCCGCCTTTTGCGCCAGCAGTACCTGTTGTTCCAGGTTGAAACTGTTGGTGTGGTA
GGCGGTAAAGTTCGCCGTCGCCGTTAGCGGCGCATAGGGCGGATCGCAATACACCACTGTGCGGCTA
TCCGCACGTTGCATGCACTCTTCGTAAGATTCGCAGTAAAACTCGGCGTTTTGCGCCTTCTCGGCGA
AATGATAGAGCTCAGCTTCGGGGAAATAGGGCTTTTTATAACGGCCAAACGGCACATTGAACTCGCC
GCGCAG

MUT46

A *Klebsiella* bacterial mutant (MUT46) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding a putative inner membrane protein (VIR46). The insertion site nucleic acid sequence identifying the VIR46 gene in MUT46 is shown in Table 48.

Table 48. MUT46 Transposon Insertion Site (SEQ ID NO:64)

TGTCAATGCGCAATTTGGTTAAATATGTCGGTATTGGCCTGCTGGTGATGGGGCTTGCCGCCTGCGA
TAACAGCGATTCAAAAGCGCCAACCGTTGGCGCAGCAGCGGAGAGCAATGCCAGCGGCCAGGCAATC
AGCCTGCTGGATGGCAAGCTGAGCTTCACCCTGCCTGCGGGCATGGCCGACCAGAGCGGCAAACTGG
GTACCCAGGCGAACAATATGCACGTCTACTCTGACGCTACCGGCCAGAAAGCGGTCATCGTCATCGT
CGGCGACAGCACCAATGA

IV. SUITABLE TARGET PATHOGENS

Other *Pseudomonas* sp. and *Klebsiella* sp. and many other microbes, including gram-negative bacterial strains, are likely to include virulence genes encoding VIRX-related peptides or proteins having amino acid sequence identity or similarity to those identified herein. Suitable bacterial pathogens may include, but are not limited to, *Pneumococci* sp., *Klebsiella*, sp., *Pseudomonas*, *e.g.*, *P. aeruginosa*, *Salmonella*, *e.g.*, *Salmonella typhimurium*, *Legionella*, *e.g.*, *Legionella pneumophilia*, *Escherichia*, *e.g.*, *Escherichia coli*, *Listeria*, *e.g.*, *Listeria monocytogenes*, *Staphylococcus*, *e.g.*, *Staphylococcus aureus*, *Streptococci* sp., *Vibrio*, *e.g.*, *Vibrio cholerae*. Pathogenic mycobacteria of the present invention may include *e.g.*, *Mycobacterium tuberculosis*. Pathogenic fungi of the present invention may include, *e.g.*, *Candida albicans*. Pathogenic unicellular eukaryotic organisms of the present invention may include, *e.g.*, *Leishmania donovani*.

Having identified VIRX genes according to the invention, it is possible to use the gene sequence to search for related genes or peptides in other microorganisms. This may be carried out by searching in existing databases, *e.g.*, EMBL or GenBank. The levels of identity between gene sequences and levels of identity or similarity between, amino acid sequences can be calculated using known methods. In relation to the present invention, publicly available computer based methods for determining identity and similarity include the BLASTP, BLASTN and FASTA (Atschul *et al.*, J. Molec. Biol., 1990; 215:403-410), the

BLASTX program available from NCBI, and the Gap program from Genetics Computer Group, Madison WI.

Preferably, the peptides that may be useful in the various aspects of the invention have greater than a 40% similarity with the peptides identified herein. More preferably, the peptides have greater than 60% sequence similarity. Most preferably, the peptides have greater than 80% sequence similarity, *e.g.*, 95% similarity. With regard to the polynucleotide sequences identified herein, related polynucleotides that may be useful in the various aspects of the invention may have greater than 40% identity with the sequences identified herein. More preferably, the polynucleotide sequences have greater than 60% sequence identity. Most preferably, the polynucleotide sequences have greater than 80% sequence identity, *e.g.*, 95% identity.

In addition to related molecules from other microorganisms, the invention encompasses modifications made to the peptides and polynucleotides identified herein which do not significantly alter the biological function. It will be apparent to the artisan that the degeneracy of the genetic code can result in polynucleotides with minor base changes from those specified herein, but which nevertheless encode the same peptides. Complementary polynucleotides are also within the invention. Conservative replacements at the amino acid level are also envisaged, *i.e.*, different acidic or basic amino acids may be substituted without substantial loss of function.

It is recognized in the art that highly refined mechanisms that regulate transcription have evolved and are present in bacteria. Most bacterial genes are organized into operons, which are groups of genes coding for related proteins. Operons can either be repressed or induced thus regulating those genes. An operon consists of an operator, promoter, regulator, and structural genes. The regulator gene codes for a repressor protein that binds to the operator, obstructing the promoter (thus, transcription) of the structural genes. The regulator does not have to be adjacent to other genes in the operon. If the repressor protein is removed, transcription may occur.

Transposon mutagenesis usually inactivates the gene in which the transposon is inserted, as well as any gene downstream in the same operon. If the VIRX gene is a structural gene in an operon, inactivation of the VIRX gene disrupts the expression of other structural genes in the same operon and positioned downstream of the inactivated VIRX gene. For example, an insertion in pchE gene also inactivates pchF, pchG, pchH, and pchI genes

because they all reside within the pchEFGHI operon and are downstream of the inactivated pchE gene. Accordingly, the present invention includes attenuation of virulence due to alteration of a VIRX gene residing in an operon as well as alterations to nucleic acid yielding loss of expression of structural genes located in the same operon and located downstream of the VIRX gene. In one embodiment, the present invention is an alteration inactivating the first gene of an operon carrying a VIRX gene of the invention. The alteration of nucleic acids of VIRX genes and VIRX-containing operons may be insertional inactivation or gene deletion. It is preferred that the alteration of nucleic acids of VIRX genes and VIRX-containing operons be insertional inactivation.

The present invention also provides for a bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein the bacterial strain includes a mutation that reduces expression of the VIRX gene relative to an isogenic bacterial strain lacking the mutation. In one embodiment, the mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking the mutation. In another embodiment, the attenuated bacterial strain has more than one mutation of an operon containing a VIRX gene when compared to an isogenic bacterial strain.

V. VIRX NUCLEIC ACIDS AND POLYPEPTIDES CAN BE USED TO IDENTIFY ANTIMICROBIAL DRUGS

A. Screening

In a separate embodiment, the VIRX genes, or their polynucleotide or polypeptide products disclosed herein is used in screening assays for the identification of potential antimicrobial drugs. Routine screening assays are known to those skilled in the art, and can be adapted using the VIRX products of the invention in the appropriate way. For example, the products of the invention can be used as the target for a potential drug, with the ability of the drug to inactivate or bind to the target indicating its potential antimicrobial activity. In the

methods of the present invention, one or more test compounds may be present or produced in the assay mixture. Preferably one compound is present, or produced, in the assay mixture.

B. Character of Antimicrobial Candidate Compositions

VIRX nucleic acids and polypeptides may be used to identify drugs or therapeutics in a candidate composition useful in the prevention or treatment of pathogen-associated disease or infection. A candidate composition can include one or more molecules for analysis in a screening assay and can be a synthetic or semi-synthetic molecules. Such molecules include inorganic as well as organic chemical molecules. The molecules may be less than about 500 Daltons or more than 500 Daltons. The molecules may be naturally occurring. Naturally occurring molecules may include, *e.g.*, saccharides, lipids, peptides, proteins, nucleic acids, or combinations thereof, *e.g.*, aminoglycosides, glycolipids, lipopolysaccharides, or macrolides. Proteins may be immunoglobulins, *e.g.*, polyclonal or monoclonal antibodies. Nucleic acids may be DNA or RNA, *e.g.*, small interfering RNA (siRNA). The precise source of the molecule is not critical to the method of the present invention. The molecule might be derived from *e.g.*, synthetic compounds libraries that are commercially available, *e.g.*, Sigma-Aldrich (Milwaukee, WI), or libraries of natural occurring molecules in the form of bacterial, fungal, plant, and animal extracts such as those available from Xenova (Slough, UK). The synthetic (or semi-synthetic) or natural occurring molecules might be modified using standard chemical, physical, or biochemical methods known in the art.

VI. VIRX NUCLEIC ACIDS AND POLYPEPTIDES CAN BE USED TO DETECT THE DEGREE OF VIRULENCE OF PATHOGENS

A diagnostic test can assist physicians in determining the type of disease and appropriate associated therapy. As such, a separate embodiment of this invention provides for the use of VIRX genes or their polynucleotides or nucleic acid products as virulence markers for detecting the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen. There are many diagnostic assay approaches known to the artisan. Generally, the diagnostic method used would comprise the steps of (a) obtaining a sample from a potentially diseased subject or a diseased subject; (b) measuring the level of at least one polypeptide or polynucleotide virulence marker in the sample; and (c) comparing the amount of the virulence marker in the sample of step (a) to the amount of the virulence

marker present in a control sample from a second subject known not to have the presence of the pathogen, where an alteration in the expression level of the virulence marker in the first subject as compared to the control sample indicates the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen. Preferably, the subject is a mammal. More preferred is that the subject is a human. The person of skill will recognize that diagnostic tests may be performed in an array-type format wherein, *e.g.*, the presence of two or more VIRX genes or gene products indicate the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen.

VII. ATTENUATED ORGANISMS OF THE PRESENT INVENTION CAN BE USED IN VACCINE PREPARATION

In another embodiment, the invention provides for the use of the attenuated organisms described herein in vaccine preparation. The preparation of vaccines based on attenuated microorganisms is known to those skilled in the art. Vaccine compositions can be formulated with suitable carriers or adjuvants, *e.g.*, alum, as necessary or desired, to provide effective immunization against infection. The preparation of vaccine formulations will be apparent to the artisan. The attenuated microorganisms may be prepared with a mutation that disrupts the expression of any of the VIRX genes identified herein. The artisan will be aware of methods for disrupting expression of particular VIRX genes. Techniques that may be used include, but are not limited to, insertional inactivation, or gene deletion techniques. Attenuated microorganisms according to the invention may also comprise additional mutations in other genes, for example in a second gene identified herein or in a separate gene required for growth of the microorganism, *e.g.*, an *Aro* mutation. Attenuated microorganisms may also be used as carrier systems for the delivery of heterologous antigens, therapeutic proteins or nucleic acids (DNA or RNA). In this embodiment, the attenuated microorganisms are used to deliver a heterologous antigen, protein or nucleic acid to a particular site *in vivo*. Introduction of a heterologous antigen, peptide or nucleic acid into an attenuated microorganism can be carried out by conventional techniques, including the use of recombinant constructs, *e.g.*, vectors, which comprise polynucleotides that express the heterologous antigen or therapeutic protein, and also include suitable promoter sequences. Alternatively, the gene that encodes the heterologous antigen or protein may be incorporated into the genome of the organism and the endogenous promoters used to control expression. In the vaccines of the present invention, the pharmaceutically effective dosage of the mutants of the present invention to be

administered may vary depending on the age, weight and sex of the subject, and the mode of administration. The subject can be, *e.g.*, a human, a non-human primate (such as an ape, gorilla, or chimpanzee), cow, horse, pig, sheep, dog, cat, or rodent (including mouse or rat).

VIII. DEFINITIONS

As used herein, each of the following terms has the meaning associated with it in this section.

The term "pathogen," as used herein, is intended to include an agent that causes disease, especially a living microorganism such as a bacterium or fungus. The terms "agent" and "factor" are used interchangeably herein to describe pathogens or toxins useful in the methods of the present invention. Pathogens may include any bacteria, mycobacteria, fungi and unicellular eukaryotic organism, including wild types and mutants thereof, which causes disease or brings about damage or harm to a host organism. Pathogens may also be a poisonous substance, *e.g.*, toxin, which is produced by living cells or organisms and is capable of causing disease when introduced to a host.

The term, "pathogenic," as used herein, is defined as an agent's ability to cause disease, damage or harm to a host organism.

The term, "attenuated," as used herein, means an organism made less virulent relative to an isogenic pathogenic organism.

The term, "virulence," as used herein, is a measure of the degree of pathogenicity of an agent to a host organism. Virulence is usually expressed as the dose of an agent or cell number of a pathogen that will elicit a pathological response in the host organism within a given time period. "Reducing the virulence" as used herein is defined as the ability of a compound to attenuate, diminish, decrease, suppress, or arrest the development of, or the progression of disease, damage or harm to a host organism mediated by a pathogen.

The term, "host organism," as used herein, is intended to include any living organism. Preferably the host organism is a eukaryote, *e.g.*, vertebrate. More preferably the host organism is a mammal. It is most preferred that the host organism be a human.

The term, "mutant," as used herein, an organism carrying a specific mutation of a gene that is expressed in the organism's phenotype.

The term, "mutation," as used herein, is an alteration of one or more nucleic acids of a polynucleotide sequence encoding a gene. A mutation may include the insertion of additional nucleic acids to a polynucleotide sequence encoding a gene, e.g., insertional inactivation of a gene. Alternatively, a mutation may include, but is not limited to, deletion of one or more nulceic acids of a polynucleotide sequence encoding a gene.

The term, "operon," as used herein, is a unit of bacterial gene expression and regulation comprising several genes usually with complementary functions. Typically an operon includes nucleic acid and control elements in the nucleic acid that may be recognized by regulators of gene products. Insertion in a gene in an operon interferes with the function of this gene and of other genes located downstream or upstream in the operon. It is understood herein that the function attributed to a gene refers to its function and/or that of any gene located downstream or upstream in the same operon.

The term, "pharmaceutically effective dosage," as used herein, means that amount necessary at least partly to attain the desired effect, or to delay the onset of, inhibit the progression of, or halt altogether, the onset or progression of the particular condition being treated.

The terms "similarity" and "identity" are known in the art. The use of the term "identity" refers to a sequence comparison based on identical matches between correspondingly identical positions in the sequences being compared. The term "similarity" refers to a comparison between amino acid sequences, and takes into account not only identical amino acids in corresponding positions, but also functionally similar amino acids in corresponding positions. Thus similarity between polypeptide sequences indicates functional similarity, in addition to sequence similarity.

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that bacterial genes have been identified and assigned a new role in virulence. Further, these genes and their products are useful in the identification of antimicrobial agents, the diagnosis of pathogen-associated disease or infection as well as the preparation of vaccines. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and

modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. For instance, the choice of the particular pathogen, or combination of pathogens selected for assay or vaccination, the test conditions used in diagnostic assays utilizing the pathogens of this invention, or the method of mutagenesis used to derive the attenuated mutants is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein.

EXAMPLES

This Example is provided for the purpose of illustration only and the invention should in no way be construed as being limited to these Example, but rather should be construed to encompass any and all variations which become evident as a result of the teaching provided.

EXAMPLE 1 STRAINS AND CULTURE CONDITIONS USED TO SCREEN FOR ATTENUATED VIURLENCE IN TEST BACTERIAL MUTANTS.

The *D. discoideum* wild-type strain DH1-10 used in these studies is a subclone of DH1 (Cornillon *et al.*, J. Biol. Chem., 275(44):34287-92, 2000). Cells were grown at 21°C in HL5 medium (14.3 g/l peptone (Oxoid), 7.15 g/l yeast extract, 18g/l maltose, 0.64 g/l $Na_2HPO_4 2H_2O$, 0.49 g/l KH_2PO_4, pH 6.7) (Cornillon *et al.*, J. Cell. Sci., 107 (Pt 10):2691-704, 1994) and subcultured twice a week.

Bacteria were grown overnight at 37°C on Luria-Bertani (LB) agar. Single colonies were inoculated into 5 ml PB (2% (wt/vol) peptone, 0.3% (wt/vol) $MgCl_2.6H_2O$, 1% (wt/vol) K_2SO_4) (Essar *et al.*, J. Bacteriol., 172(2):884-900,1990) in a 50 ml flask and grown at 37°C for 8 hr prior to use. The growth of various strains was tested in rich medium (PB) by measuring the optical density (600 nm) of a culture at different times after inoculation and was found to be comparable for all strains used. Under these conditions, similar OD_{600s} were obtained for each strain and the induction of quorum sensing was maximal. Minimal Inhibitory Concentrations (MICs) were determined in Mueller-Hinton broth by the microdilution method (Thornsberry *et al.*, NCCLS, 3: 48-56, 1983). Mutations yielding reduced virulence were identified where the growth of the *Dictyostelium* test host organism exposed to the mutant pathogen was greater than the *Dictyostelium* test host organism exposed to wild-type pathogen. Specific genetic mutations in pathogens displaying reduced virulence were identified and characterized by techniques well know in the art.

CLAIMS

What is claimed is:

1. An attenuated bacterial mutant derived from a pathogenic bacterial strain, wherein said attenuated mutant has:

(i) a mutation of a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and

(ii) reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain.

2. An attenuated bacterial mutant of claim 1, wherein said mutation is insertional inactivation or a gene deletion.

3. An attenuated bacterial mutant of claim 1, wherein said mutant is a gram-negative bacteria.

4. An attenuated bacterial mutant of claim 3, wherein said attenuated gram-negative bacterial mutant is a *Pseudomonas* species.

5. An attenuated bacterial mutant of claim 4, wherein said *Pseudomonas* species is *Pseudomonas aeruginosa*.

6. An attenuated *Pseudomonas* mutant of claim 5, wherein said attenuated *Pseudomonas* mutant is selected from the group consisting of: MUT1; MUT2; MUT3; MUT4; MUT5; MUT6; MUT7; MUT8; MUT9; MUT10; MUT11; MUT12; MUT13; MUT14; MUT15; MUT16; MUT17; MUT18; and MUT19.

7. An attenuated bacterial mutant of claim 3, wherein said gram-negative bacterial mutant is a *Klebsiella* species.

8. An attenuated bacterial mutant of claim 7, wherein said *Klebsiella* species is *Klebsiella pneumoniae.*

9. An attenuated *Klebsiella* mutant of claim 8, wherein said attenuated *Klebsiella* mutant is selected from the group consisting of: MUT20; MUT21; MUT22; MUT23; MUT24; MUT25; MUT26; MUT27; MUT28; MUT29; MUT30; MUT31; MUT32; MUT33; MUT34; MUT35; MUT36; MUT37; MUT38; MUT39; MUT40; MUT41; MUT42; MUT43; MUT44; MUT45; and MUT46.

10. A method for identifying an antimicrobial drug, said method comprising:

(a) contacting a candidate composition with at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45 and VIR46; and

(b) comparing the biological activity of said polypeptide in the presence and absence of said candidate composition, wherein alteration of the biological activity of said polypeptide indicates that said candidate composition is an antimicrobial drug.

11. A method of claim 10, wherein said candidate composition contains at least two molecules.

12. A method of claim 10, wherein said candidate composition contains at least one molecule less than about 500 Daltons.

13. A method of claim 10, wherein said candidate composition contains at least one molecule greater than about 500 Daltons.

14. A method of claim 10, wherein said candidate composition contains at least one molecule selected from a group consisting of a polypeptide, polysaccharide, lipid, nucleic acid, or combination thereof.

15. A composition of claim 14, wherein said polypeptide is an immunoglobulin.

16. A method for identifying an antimicrobial drug, said method comprising:

(a) contacting at a candidate composition with at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and

(b) comparing the expression of said polynucleotide in the presence and absence of said candidate composition, wherein alteration of the expression of said nucleotide indicates that said candidate composition is an antimicrobial drug.

17. A method of claim 16, wherein said candidate composition contains at least two molecules.

18. A method of claim 16, wherein said candidate composition contains at least one molecule less than about 500 Daltons.

19. A method of claim 16, wherein said candidate composition contains at least one molecule greater than about 500 Daltons.

20. A method of claim 16, wherein said candidate composition contains at least one molecule selected from a group consisting of a polypeptide, polysaccharide, lipid, nucleic acid, or combination thereof.

21. A composition of claim 20, wherein said nucleic acid is a ribonucleic acid.

22. A nucleic acid of claim 21, wherein said nucleic acid is a small interfering ribonucleic acid.

23. A method for determining the degree of virulence of a pathogen in a subject, said method comprising:

(a) measuring the level of expression of at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of said polypeptide in said sample of step (a) to the amount of said polypeptide present in a control sample from a second subject known not to have the presence of said pathogen, wherein an alteration in the expression level of said polypeptide in said first subject as compared to said control sample indicates the degree of virulence of said pathogen.

24. A method of claim 23, wherein said subject is a mammal.

25. A mammalian subject of claim 24, wherein said mammalian subject is a human.

26. A method for determining the degree of virulence of a pathogen in a subject, said method comprising:

(a) measuring the level of expression of at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of said polynucleotide in said sample of step (a) to the amount of said polynucleotide present in a control sample from a second subject known not to have the presence of said pathogen, wherein an alteration in the expression level of said polynucleotide in said first subject as compared to said control sample indicates the degree of virulence of said pathogen.

27. A method of claim 26, wherein said subject is a mammal.

28. A mammalian subject of claim 27, wherein said mammalian subject is a human.

29. An attenuated bacterial mutant of claim 1, wherein said mutant encodes and expresses a foreign antigen.

30. An attenuated bacterial mutant of claim 1, wherein said mutant contains a plasmid which encodes and expresses, in a eukaryotic cell, a foreign antigen.

31. A vaccine against a disease caused by a pathogenic microorganism comprising:

(a) a pharmaceutically effective dosage of one or more of the attenuated bacterial mutants of claim 1 and;

(b) a pharmaceutically acceptable diluent or carrier.

32. An attenuated bacterial mutant derived from a pathogenic bacterial strain, wherein said attenuated mutant has:

(i) a mutation of a gene selected from the group consisting of pchE, pchF, pchG, pchH, and pchI; and

(ii) reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain.

33. A bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein said bacterial strain includes a mutation that reduces expression of said gene relative to an isogenic bacterial strain lacking said mutation.

34. A bacterial strain of claim 33, wherein said mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking said mutation.

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Met Val Asp Lys Leu Thr His Leu Lys Gln Leu Glu Ala Glu Ser Ile
1 5 10 15

His Ile Ile Arg Glu Val Ala Ala Glu Phe Asp Asn Pro Val Met Leu
20 25 30

Tyr Ser Ile Gly Lys Asp Ser Ala Val Met Leu His Leu Ala Arg Lys
35 40 45

Ala Phe Phe Pro Gly Lys Leu Pro Phe Pro Val Met His Val Asp Thr
50 55 60

Arg Trp Lys Phe Gln Glu Met Tyr Arg Phe Arg Asp Arg Met Val Glu
65 70 75 80

Glu Met Gly Leu Asp Leu Ile Thr His Val Asn Pro Asp Gly Val Ala
85 90 95

Gln Gly Ile Asn Pro Phe Thr His Gly Ser Ala Lys His Thr Asp Val
100 105 110

Met Lys Thr Glu Gly Leu Lys Gln Ala Leu Asp Lys Tyr Gly Phe Asp
115 120 125

Ala Ala Phe Gly Gly Ala Arg Arg Asp Glu Glu Lys Ser Arg Ala Lys
130 135 140

Glu Arg Val Tyr Ser Phe Arg Asp Ser Lys His Arg Trp Asp Pro Lys
145 150 155 160

Asn Gln Arg Pro Glu Leu Trp Asn Ile Tyr Asn Gly Lys Val Lys Lys
165 170 175

Gly Glu Ser Ile Arg Val Phe Pro Leu Ser Asn Trp Thr Glu Leu Asp
180 185 190

Ile Trp Gln Tyr Ile Tyr Leu Glu Gly Ile Pro Ile Val Pro Leu Tyr
195 200 205

Phe Ala Ala Glu Arg Glu Val Ile Glu Lys Asn Gly Thr Leu Ile Met
210 215 220

Ile Asp Asp Glu Arg Ile Leu Glu His Leu Ser Asp Glu Glu Lys Ala

225 230 235 240

Arg Ile Glu Lys Arg Met Val Arg Phe Arg Thr Leu Gly Cys Tyr Pro
245 250 255

Leu Thr Gly Ala Val Glu Ser Ser Ala Thr Thr Leu Pro Glu Ile Ile
260 265 270

Gln Glu Met Leu Leu Thr Arg Thr Ser Glu Arg Gln Gly Arg Val Ile
275 280 285

Asp His Asp Gln Ala Gly Ser Met Glu Glu Lys Lys Arg Gln Gly Tyr
290 295 300

Phe
305

<210> 5
<211> 822
<212> DNA
<213> Pseudomonas aeruginosa

<400> 5
atgaggccgg tgccttgggg cgaattggtg gcgctggtgc ggcgcgccgg cgaggcgatc 60

ctgccgcact ggcgcgccga cgtggtggtg cgctcgaagg ccgacgaatc gccggtgact 120

gccgccgacc tggccgcgca ccatatattg gaggcgggat tgcgggcgct ggcgccggac 180

attccggtgc tttccgaaga ggattgcgag ataccgctga gcgagcgcgg ccactggcgg 240

cgctggtggc tggtggaccc gctggacggc accaaggagt tcatctccgg tagcgaggag 300

ttcaccgtca acgtggccct ggtcgaggat ggccgggtgc tgttcggcct ggtcggcgtg 360

ccggtgagcg gccgctgcta ctacggtggc gccggtctcg gtgcctggcg cgaggaggcc 420

gatggccgcg cgcaaccgat cagtgtgcgc ctggagcccg aggaggcctt caccgtggtg 480

gccagcaagc gccatggcag cccggcccag gagcgcctgc tggatggctt gagcgagcgc 540

ttcggcgacc tgcggcgagc cagcatcggc agttcgctga agttctgcct gctggccgag 600

ggcgctgccg actgctatcc gcgcctgacg ccaacctcgc aatgggacac ggccgccgcc 660

cagggtgtgc tggaaggcgc cggcggcgag gtgctcgacc tgcatggtgc gccattcacc 720

tacgagccgc gcgaggatta cctcaacggc tccttcctgg ccctgccgcg cgccgccgag 780

tggcgcagcg agctgatcca actggcgcgc gcgctgcact ga 822

<210> 6
<211> 273
<212> PRT
<213> Pseudomonas aeruginosa

<400> 6

Met Arg Pro Val Pro Trp Gly Glu Leu Val Ala Leu Val Arg Arg Ala
1 5 10 15

Gly Glu Ala Ile Leu Pro His Trp Arg Ala Asp Val Val Val Arg Ser
20 25 30

Lys Ala Asp Glu Ser Pro Val Thr Ala Ala Asp Leu Ala Ala His His
35 40 45

Ile Leu Glu Ala Gly Leu Arg Ala Leu Ala Pro Asp Ile Pro Val Leu
50 55 60

Ser Glu Glu Asp Cys Glu Ile Pro Leu Ser Glu Arg Gly His Trp Arg
65 70 75 80

Arg Trp Trp Leu Val Asp Pro Leu Asp Gly Thr Lys Glu Phe Ile Ser
85 90 95

Gly Ser Glu Glu Phe Thr Val Asn Val Ala Leu Val Glu Asp Gly Arg
100 105 110

Val Leu Phe Gly Leu Val Gly Val Pro Val Ser Gly Arg Cys Tyr Tyr
115 120 125

Gly Gly Ala Gly Leu Gly Ala Trp Arg Glu Glu Ala Asp Gly Arg Ala
130 135 140

Gln Pro Ile Ser Val Arg Leu Glu Pro Glu Glu Ala Phe Thr Val Val
145 150 155 160

Ala Ser Lys Arg His Gly Ser Pro Ala Gln Glu Arg Leu Leu Asp Gly
165 170 175

Leu Ser Glu Arg Phe Gly Asp Leu Arg Arg Ala Ser Ile Gly Ser Ser
180 185 190

Leu Lys Phe Cys Leu Leu Ala Glu Gly Ala Ala Asp Cys Tyr Pro Arg
195 200 205

Leu Thr Pro Thr Ser Gln Trp Asp Thr Ala Ala Ala Gln Gly Val Leu
210 215 220

Glu Gly Ala Gly Gly Glu Val Leu Asp Leu His Gly Ala Pro Phe Thr
225 230 235 240

Tyr Glu Pro Arg Glu Asp Tyr Leu Asn Gly Ser Phe Leu Ala Leu Pro
245 250 255

Arg Ala Ala Glu Trp Arg Ser Glu Leu Ile Gln Leu Ala Arg Ala Leu
260 265 270

His

<210> 7
<211> 1299
<212> DNA
<213> Pseudomonas aeruginosa

<400> 7
atgcgagttc tggtccttgg cagcggtgtc atcggtaccg ccagtgcgta ttacctggcc 60

cgtgccgggt tcgaggtggt ggtggtcgac cgtcaggacg gtcccgcgct ggaaaccagc 120

ttcgccaacg ccggccaggt gtctcccggc tacgcttcgc cctgggcagc cccgggcatt 180

cccctgaagg ccatgaagtg gctgctggaa aagcacgcgc cgctggccat caagctcacc 240

tccgatccca gccagtacgc ctggatgctg cagatgctgc gcaactgcac cgccgagcgc 300

tacgccgtga acaaggagcg catggtccgc ctgtccgagt acagccgcga ttgcctcgac 360

gaactgcgcg ccgagaccgg catcgcctac gagggccgca ccctcggcac cacccaactg 420

ttccgcaccc aggcgcagct ggacgccgcc ggcaaggaca tcgccgtgct cgagcgctcc 480

ggcgtgccct acgaggttct cgaccgcgac ggcatcgccc gcgtagagcc ggctttggcc 540

aaggtcgccg acaagctggt cggcgccttg cgcctgccca acgaccagac cggcgactgc 600

cagctgttca ccacccgcct ggcggaaatg gccaagggcc tgggcgtgga gttccgcttc 660

ggccagaaca tcgagcgcct ggacttcgcc ggcgaccgca tcaacggcgt gctggtcaac 720

ggcgaattgc tcaccgccga ccactacgtg ctggccctgg gcagctactc gccgcaactg 780

ctcaagccgc tgggtatcaa ggctccggtc tatccgctga agggttattc gctgaccgtg 840

ccgatcacca acccggagat ggcgccgacc tcgaccatcc tcgacgagac ctacaaggtg 900

gcgatcaccc gcttcgacca gcgcatccgc gtcggcggca tggcggaaat cgccggcttc 960

gacctgtcgc tgaacccgcg ccgccgcgag accctggaaa tgatcaccac cgacctctat 1020

cccgagggcg gcgatatcag ccaggcgacc ttctggaccg gcctgcgccc ggcgaccccg 1080

gatggcaccc cgatcgtcgg cgccacccgc taccgcaacc tgttcctcaa taccggccac 1140

ggcaccctgg gttggaccat ggcctgcggg tcgggtcgct acctggccga cctgatggcg 1200

aagaagcgcc cgcagatcag taccgaaggc ctggatattt cccgctacag caattccccg 1260

gagaacgcca agaatgccca tccagcgcca gcacactaa 1299

<210> 8
<211> 432
<212> PRT
<213> Pseudomonas aeruginosa

<400> 8

Met Arg Val Leu Val Leu Gly Ser Gly Val Ile Gly Thr Ala Ser Ala
1 5 10 15

Tyr Tyr Leu Ala Arg Ala Gly Phe Glu Val Val Val Val Asp Arg Gln
20 25 30

Asp Gly Pro Ala Leu Glu Thr Ser Phe Ala Asn Ala Gly Gln Val Ser
35 40 45

Pro Gly Tyr Ala Ser Pro Trp Ala Ala Pro Gly Ile Pro Leu Lys Ala
50 55 60

Met Lys Trp Leu Leu Glu Lys His Ala Pro Leu Ala Ile Lys Leu Thr
65 70 75 80

Ser Asp Pro Ser Gln Tyr Ala Trp Met Leu Gln Met Leu Arg Asn Cys
85 90 95

Thr Ala Glu Arg Tyr Ala Val Asn Lys Glu Arg Met Val Arg Leu Ser
100 105 110

Glu Tyr Ser Arg Asp Cys Leu Asp Glu Leu Arg Ala Glu Thr Gly Ile
115 120 125

Ala Tyr Glu Gly Arg Thr Leu Gly Thr Thr Gln Leu Phe Arg Thr Gln
130 135 140

Ala Gln Leu Asp Ala Ala Gly Lys Asp Ile Ala Val Leu Glu Arg Ser
145 150 155 160

Gly Val Pro Tyr Glu Val Leu Asp Arg Asp Gly Ile Ala Arg Val Glu
165 170 175

Pro Ala Leu Ala Lys Val Ala Asp Lys Leu Val Gly Ala Leu Arg Leu
180 185 190

Pro Asn Asp Gln Thr Gly Asp Cys Gln Leu Phe Thr Thr Arg Leu Ala
195 200 205

Glu Met Ala Lys Gly Leu Gly Val Glu Phe Arg Phe Gly Gln Asn Ile
210 215 220

Glu Arg Leu Asp Phe Ala Gly Asp Arg Ile Asn Gly Val Leu Val Asn
225 230 235 240

Gly Glu Leu Leu Thr Ala Asp His Tyr Val Leu Ala Leu Gly Ser Tyr

245 250 255

Ser Pro Gln Leu Leu Lys Pro Leu Gly Ile Lys Ala Pro Val Tyr Pro
260 265 270

Leu Lys Gly Tyr Ser Leu Thr Val Pro Ile Thr Asn Pro Glu Met Ala
275 280 285

Pro Thr Ser Thr Ile Leu Asp Glu Thr Tyr Lys Val Ala Ile Thr Arg
290 295 300

Phe Asp Gln Arg Ile Arg Val Gly Gly Met Ala Glu Ile Ala Gly Phe
305 310 315 320

Asp Leu Ser Leu Asn Pro Arg Arg Arg Glu Thr Leu Glu Met Ile Thr
325 330 335

Thr Asp Leu Tyr Pro Glu Gly Gly Asp Ile Ser Gln Ala Thr Phe Trp
340 345 350

Thr Gly Leu Arg Pro Ala Thr Pro Asp Gly Thr Pro Ile Val Gly Ala
355 360 365

Thr Arg Tyr Arg Asn Leu Phe Leu Asn Thr Gly His Gly Thr Leu Gly
370 375 380

Trp Thr Met Ala Cys Gly Ser Gly Arg Tyr Leu Ala Asp Leu Met Ala
385 390 395 400

Lys Lys Arg Pro Gln Ile Ser Thr Glu Gly Leu Asp Ile Ser Arg Tyr
405 410 415

Ser Asn Ser Pro Glu Asn Ala Lys Asn Ala His Pro Ala Pro Ala His
420 425 430

<210> 9
<211> 771
<212> DNA
<213> Pseudomonas aeruginosa

<400> 9
atggcactgg caaaacgcat catcccctgc ctcgacgtgg acaacggccg agtggtcaag 60

ggcgtcaagt tcgagaacat ccgcgacgcc ggcgacccgg tcgagatcgc tcgccgctac 120

gacgagcagg gtgccgacga gatcaccttc ctcgatatca ccgccagcgt cgacgggcgc 180

gacaccaccc tgcataccgt cgagcgcatg gctagccagg tgttcattcc gctgaccgtg 240

ggcggcggcg tacgcagcgt gcaggacatc cgcaacctgt tgaatgccgg cgcggacaag 300

gtctcgatca acaccgccgc ggtgttcaac cccgagttcg tcggtgaggc cgccgaccgc 360

ttcggctcgc agtgcatcgt ggtcgccatc gacgcgaaga aggtttccgc cccgggcgag 420

gcgccgcgct gggaaatctt cacccatggc gggcgcaagc ccaccgggct ggatgccgtg 480

ctctgggcga agaagatgga agacttgggc gctggcgaga ttctcctgac cagcatggac 540

caggacggcg tgaagagcgg ttacgacctg ggcgtgaccc gcgccatcag cgaggcggtg 600

aacgtgccgg tgatcgcttc cggcggcgtc ggcaacctgg agcacctggc cgccggcatc 660

ctcgagggca aggccgacgc ggtgctcgcg gcgagcatct tccacttcgg cgagtacacc 720

gtgccggaag ccaaggccta cctggccagc cgcggtatcg tggtgcgctg a 771

<210> 10
<211> 256
<212> PRT
<213> Pseudomonas aeruginosa

<400> 10

Met Ala Leu Ala Lys Arg Ile Ile Pro Cys Leu Asp Val Asp Asn Gly
1 5 10 15

Arg Val Val Lys Gly Val Lys Phe Glu Asn Ile Arg Asp Ala Gly Asp
20 25 30

Pro Val Glu Ile Ala Arg Arg Tyr Asp Glu Gln Gly Ala Asp Glu Ile
35 40 45

Thr Phe Leu Asp Ile Thr Ala Ser Val Asp Gly Arg Asp Thr Thr Leu
50 55 60

His Thr Val Glu Arg Met Ala Ser Gln Val Phe Ile Pro Leu Thr Val
65 70 75 80

Gly Gly Gly Val Arg Ser Val Gln Asp Ile Arg Asn Leu Leu Asn Ala
85 90 95

Gly Ala Asp Lys Val Ser Ile Asn Thr Ala Ala Val Phe Asn Pro Glu
100 105 110

Phe Val Gly Glu Ala Ala Asp Arg Phe Gly Ser Gln Cys Ile Val Val
115 120 125

Ala Ile Asp Ala Lys Lys Val Ser Ala Pro Gly Glu Ala Pro Arg Trp
130 135 140

Glu Ile Phe Thr His Gly Gly Arg Lys Pro Thr Gly Leu Asp Ala Val
145 150 155 160

Leu Trp Ala Lys Lys Met Glu Asp Leu Gly Ala Gly Glu Ile Leu Leu

165 170 175

Thr Ser Met Asp Gln Asp Gly Val Lys Ser Gly Tyr Asp Leu Gly Val
180 185 190

Thr Arg Ala Ile Ser Glu Ala Val Asn Val Pro Val Ile Ala Ser Gly
195 200 205

Gly Val Gly Asn Leu Glu His Leu Ala Ala Gly Ile Leu Glu Gly Lys
210 215 220

Ala Asp Ala Val Leu Ala Ala Ser Ile Phe His Phe Gly Glu Tyr Thr
225 230 235 240

Val Pro Glu Ala Lys Ala Tyr Leu Ala Ser Arg Gly Ile Val Val Arg
245 250 255

<210> 11
<211> 1035
<212> DNA
<213> Pseudomonas aeruginosa

<400> 11
atgatcaagg tcggcatcgt tggcggtacg ggttatacgg gcgtggaact gctgcgcctg 60

ctggcgcagc atccgcaggc ccgggtggaa gtgatcactt cgcgttccga ggcgggggtg 120

aaggtcgccg acatgtaccc gaacctgcga ggtcattatg acgacctgca gttcagcgtg 180

ccggacgcgc agcgcctcgg cgcctgcgac gtggtgttct tcgccacgcc gcacggcgtg 240

gcgcacgcgc tggctggcga actgctggac gccgggaccc gggtcatcga tctgtccgct 300

gacttccgcc tggcggacgc cgaggagtgg gcgcgctggt acggccagcc gcatggcgct 360

ccggcgctgc tcgacgaggc tgtctacggc ctgccggaag tgaaccgcga gaagatccgc 420

caggcccgcc tgatcgccgt gccgggctgc tacccgaccg cgacccagct gggcctgatc 480

ccgctgctgg aagccggcct ggccgacgcc tcgcggctga tcgccgattg caagtccggg 540

gtcagcggtg ccggtcgggg cgccaaggtt ggctcgctgt tctgcgaggc gggcgaaagc 600

atgatggcct acgcggtcaa agggcatcgg catctcccgg aaatcagcca gggcctgcgt 660

cgggcctccg gcggcgacgt cgggctgacg ttcgtaccgc acctgacgcc aatgatccgc 720

ggtatccatg caaccctcta tgcccatgtc gcggatcgct cggtcgacct ccaggcgttg 780

ttcgagaagc gctacgccga cgaacccttc gtcgacgtga tgccggccgg cagccatccg 840

gagacccgca gcgtgcgtgg cgccaatgtc tgccgaatcg ccgtgcatcg cccccagggc 900

ggcgacctgg tggtggtgct gtcggtgatc gacaacctgg tcaagggcgc ctcgggtcag 960

gcgctccaga acatgaacat cctgttcggg ctggacgagc gcctgggcct ctcgcatgcg 1020

gccctgctcc cctga 1035

<210> 12
<211> 344
<212> PRT
<213> Pseudomonas aeruginosa

<400> 12

Met Ile Lys Val Gly Ile Val Gly Gly Thr Gly Tyr Thr Gly Val Glu
1 5 10 15

Leu Leu Arg Leu Leu Ala Gln His Pro Gln Ala Arg Val Glu Val Ile
20 25 30

Thr Ser Arg Ser Glu Ala Gly Val Lys Val Ala Asp Met Tyr Pro Asn
35 40 45

Leu Arg Gly His Tyr Asp Asp Leu Gln Phe Ser Val Pro Asp Ala Gln
50 55 60

Arg Leu Gly Ala Cys Asp Val Val Phe Phe Ala Thr Pro His Gly Val
65 70 75 80

Ala His Ala Leu Ala Gly Glu Leu Leu Asp Ala Gly Thr Arg Val Ile
85 90 95

Asp Leu Ser Ala Asp Phe Arg Leu Ala Asp Ala Glu Glu Trp Ala Arg
100 105 110

Trp Tyr Gly Gln Pro His Gly Ala Pro Ala Leu Leu Asp Glu Ala Val
115 120 125

Tyr Gly Leu Pro Glu Val Asn Arg Glu Lys Ile Arg Gln Ala Arg Leu
130 135 140

Ile Ala Val Pro Gly Cys Tyr Pro Thr Ala Thr Gln Leu Gly Leu Ile
145 150 155 160

Pro Leu Leu Glu Ala Gly Leu Ala Asp Ala Ser Arg Leu Ile Ala Asp
165 170 175

Cys Lys Ser Gly Val Ser Gly Ala Gly Arg Gly Ala Lys Val Gly Ser
180 185 190

Leu Phe Cys Glu Ala Gly Glu Ser Met Met Ala Tyr Ala Val Lys Gly
195 200 205

His Arg His Leu Pro Glu Ile Ser Gln Gly Leu Arg Arg Ala Ser Gly
210 215 220

Gly Asp Val Gly Leu Thr Phe Val Pro His Leu Thr Pro Met Ile Arg
225 230 235 240

Gly Ile His Ala Thr Leu Tyr Ala His Val Ala Asp Arg Ser Val Asp
245 250 255

Leu Gln Ala Leu Phe Glu Lys Arg Tyr Ala Asp Glu Pro Phe Val Asp
260 265 270

Val Met Pro Ala Gly Ser His Pro Glu Thr Arg Ser Val Arg Gly Ala
275 280 285

Asn Val Cys Arg Ile Ala Val His Arg Pro Gln Gly Gly Asp Leu Val
290 295 300

Val Val Leu Ser Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly Gln
305 310 315 320

Ala Leu Gln Asn Met Asn Ile Leu Phe Gly Leu Asp Glu Arg Leu Gly
325 330 335

Leu Ser His Ala Ala Leu Leu Pro
340

<210> 13
<211> 1644
<212> DNA
<213> Pseudomonas aeruginosa

<400> 13
gtgagcgaac tcattcgcgt acccgacatc ggcaacggtg agggtgaagt catcgagctg 60

ctggtcaagc ccggcgacaa ggtcgaggcc gatcagagcc tgctgaccct ggaatccgac 120

aaggccagca tggaaatccc cagtcccaag gccggggtag tgaaaagcat caaggcgaag 180

gtcggcgaca ccttgaaaga aggtgacgaa atcctcgagc tggaagtgga aggcggcgaa 240

cagcctgccg aagccaaggc cgaggcagcg cccgcccaac cggaagcgcc gaaagccgaa 300

gcgcctgctc ccgccccgag cgagagcaag ccggccgccc ccgccgcggc cagcgtccag 360

gacatcaagg tcccggacat cggctcggcc ggcaaggcca acgtcatcga agtgatggtc 420

aaggccggcg acacggtcga ggccgaccag tcgctgatca ccctggaatc cgacaaggcc 480

agcatggaga tcccctcgcc ggcctccggg gtggtggaaa gcgtctcgat caaggtcggt 540

gacgaagtcg gcaccggcga cctgatcctc aagctgaagg tggaaggcgc cgctccggca 600

gccgaagagc aaccggcagc cgctccggcc caggccgcgg cgcccgccgc cgagcagaag 660

cccgccgcgg cggcccctgc gccagccaag gccgataccc cggctccggt cggcgcaccc 720

agccgcgacg gcgccaaggt ccacgccggc ccggcggtgc gcatgctggc gcgcgagttc 780

ggcgtcgagc tgagcgaagt gaaagccagc ggtcccaagg gtcgcatcct caaggaagac 840

gtccaggcct tcgtcaagga gcaactgcag cgcgccaagt ccggcggtgc cggcgccacc 900

ggcggagccg gcatcccgcc gatcccggaa gtcgacttca gcaagttcgg cgaagtggaa 960

gaagtggcga tgacccgcct gatgcaggtc ggcgccgcca acctgcatcg cagctggctg 1020

aacgtgccgc acgtgaccca gttcgaccag tcggacatca ccgacatgga agccttccgc 1080

gttgcccaga aggccgcggc ggagaaggcc ggggtcaagc tgaccgtact gccgatcctg 1140

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agcggcaagg cgctgatccg caagaagtac gtacacatcg gcttcgccgt ggacactccg 1260

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cagggcgcct gcttcaccat ctccagtctc ggccacatcg gcggcaccgg cttcacgccg 1440

atcgtcaacg cgccggaagt ggcgatcctc ggtgtgtcca aggcgaccat gcagccggta 1500

tgggacggca aggccttcca gccgcgcctg atgctgccgc tgtcgctgtc ctacgaccat 1560

cgcgtgatca acggtgccgc cgcggcgcgc ttcaccaagc gcctgggcga gctgctggcg 1620

gacatccgca ccctgctcct gtaa 1644

<210> 14
<211> 547
<212> PRT
<213> Pseudomonas aeruginosa

<400> 14

Met Ser Glu Leu Ile Arg Val Pro Asp Ile Gly Asn Gly Glu Gly Glu
1 5 10 15

Val Ile Glu Leu Leu Val Lys Pro Gly Asp Lys Val Glu Ala Asp Gln
20 25 30

Ser Leu Leu Thr Leu Glu Ser Asp Lys Ala Ser Met Glu Ile Pro Ser
35 40 45

Pro Lys Ala Gly Val Val Lys Ser Ile Lys Ala Lys Val Gly Asp Thr
50 55 60

Leu Lys Glu Gly Asp Glu Ile Leu Glu Leu Glu Val Glu Gly Gly Glu
65 70 75 80

Gln Pro Ala Glu Ala Lys Ala Glu Ala Ala Pro Ala Gln Pro Glu Ala
85 90 95

Pro Lys Ala Glu Ala Pro Ala Pro Ala Pro Ser Glu Ser Lys Pro Ala

100 105 110

Ala Pro Ala Ala Ala Ser Val Gln Asp Ile Lys Val Pro Asp Ile Gly
115 120 125

Ser Ala Gly Lys Ala Asn Val Ile Glu Val Met Val Lys Ala Gly Asp
130 135 140

Thr Val Glu Ala Asp Gln Ser Leu Ile Thr Leu Glu Ser Asp Lys Ala
145 150 155 160

Ser Met Glu Ile Pro Ser Pro Ala Ser Gly Val Val Glu Ser Val Ser
165 170 175

Ile Lys Val Gly Asp Glu Val Gly Thr Gly Asp Leu Ile Leu Lys Leu
180 185 190

Lys Val Glu Gly Ala Ala Pro Ala Ala Glu Glu Gln Pro Ala Ala Ala
195 200 205

Pro Ala Gln Ala Ala Ala Pro Ala Ala Glu Gln Lys Pro Ala Ala Ala
210 215 220

Ala Pro Ala Pro Ala Lys Ala Asp Thr Pro Ala Pro Val Gly Ala Pro
225 230 235 240

Ser Arg Asp Gly Ala Lys Val His Ala Gly Pro Ala Val Arg Met Leu
245 250 255

Ala Arg Glu Phe Gly Val Glu Leu Ser Glu Val Lys Ala Ser Gly Pro
260 265 270

Lys Gly Arg Ile Leu Lys Glu Asp Val Gln Val Phe Val Lys Glu Gln
275 280 285

Leu Gln Arg Ala Lys Ser Gly Gly Ala Gly Ala Thr Gly Gly Ala Gly
290 295 300

Ile Pro Pro Ile Pro Glu Val Asp Phe Ser Lys Phe Gly Glu Val Glu
305 310 315 320

Glu Val Ala Met Thr Arg Leu Met Gln Val Gly Ala Ala Asn Leu His
325 330 335

Arg Ser Trp Leu Asn Val Pro His Val Thr Gln Phe Asp Gln Ser Asp
340 345 350

Ile Thr Asp Met Glu Ala Phe Arg Val Ala Gln Lys Ala Ala Ala Glu

355 360 365

Lys Ala Gly Val Lys Leu Thr Val Leu Pro Ile Leu Leu Lys Ala Cys
370 375 380

Ala His Leu Leu Lys Glu Leu Pro Asp Phe Asn Ser Ser Leu Ala Pro
385 390 395 400

Ser Gly Lys Ala Leu Ile Arg Lys Lys Tyr Val His Ile Gly Phe Ala
405 410 415

Val Asp Thr Pro Asp Gly Leu Leu Val Pro Val Ile Arg Asp Val Asp
420 425 430

Arg Lys Ser Leu Leu Gln Leu Ala Ala Glu Ala Ala Asp Leu Ala Asp
435 440 445

Lys Ala Arg Asn Lys Lys Leu Ser Ala Asp Ala Met Gln Gly Ala Cys
450 455 460

Phe Thr Ile Ser Ser Leu Gly His Ile Gly Gly Thr Gly Phe Thr Pro
465 470 475 480

Ile Val Asn Ala Pro Glu Val Ala Ile Leu Gly Val Ser Lys Ala Thr
485 490 495

Met Gln Pro Val Trp Asp Gly Lys Ala Phe Gln Pro Arg Leu Met Leu
500 505 510

Pro Leu Ser Leu Ser Tyr Asp His Arg Val Ile Asn Gly Ala Ala Ala
515 520 525

Ala Arg Phe Thr Lys Arg Leu Gly Glu Leu Leu Ala Asp Ile Arg Thr
530 535 540

Leu Leu Leu
545

<210> 15
<211> 996
<212> DNA
<213> Pseudomonas aeruginosa

<400> 15
atgagttggc tgactcccgc tctggtcacc atcatcctca ccgtggtcaa ggccatcgtg 60

gtgctgctcg ccgtggtcat ctgcggcgcc ctgctaagct gggtcgagcg ccgcctgctc 120

ggcctctggc aggaccgcta cggccccaac cgggtcggtc cgttcggtgc gttccagctc 180

ggcgcggaca tggtcaagat gttcttcaag gaggactgga ccccgccgtt cgccgacaag 240

atgatcttca ccctggcccc ggtaatcgcg atgggcgccc tgctcgtcgc cttcgccatc 300

gtgccgatca cccccacctg gggcgtggcg gacctgaaca tcggcatcct gttcttcttc 360

gccatggccg gcctgacggt gtacgccgtg ctgttcgccg gctggtcgag caacaacaag 420

ttcgccctgc tcggcagcct gcgcgcctcg gcccagacca tctcctacga ggtgttcctg 480

gccctgtcgc tgatgggcat cgtcgcccag gtcggctcgt tcaacatgcg cgacatcgtc 540

cagtaccaga tcgacaacgt ctggttcatc attccgcagt tcttcggctt ctgcaccttc 600

atcatcgccg gcgtcgccgt gacccaccgt cacccgttcg accagccgga agcggagcag 660

gaactggcgg acggctacca catcgagtac gccgggatga aatggggcat gttcttcgtc 720

ggcgagtaca tcggcatcgt actggtctcg gcgctgctgg cgaccctgtt cttcggcggc 780

tggcacggtc cgttcctgga caccctgccc tggctgtcgt tcttctactt cgccgccaag 840

accggcttct tcatcatgct cttcatcctg atccgcgcct cgctgccgcg tccgcgctat 900

gaccaggtga tggcgttcag ctggaaggtg tgcctgccgc tgaccctgat caacctgctg 960

gtgaccggcg cgctcgtgct ggccgcggcc cagtaa 996

<210> 16
<211> 331
<212> PRT
<213> Pseudomonas aeruginosa

<400> 16

Met Ser Trp Leu Thr Pro Ala Leu Val Thr Ile Ile Leu Thr Val Val
1 5 10 15

Lys Ala Ile Val Val Leu Leu Ala Val Val Ile Cys Gly Ala Leu Leu
20 25 30

Ser Trp Val Glu Arg Arg Leu Leu Gly Leu Trp Gln Asp Arg Tyr Gly
35 40 45

Pro Asn Arg Val Gly Pro Phe Gly Ala Phe Gln Leu Gly Ala Asp Met
50 55 60

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Leu Asn Ala Arg Ala Asn Arg Leu Ala His Cys Leu Ile Ala Arg
1595 1600 1605

Gly Val Gly Ala Asp Val Pro Val Gly Leu Ala Leu Glu Arg Ser
1610 1615 1620

Leu Asp Met Leu Val Gly Leu Leu Ala Ile Leu Lys Ala Gly Gly
1625 1630 1635

Ala Tyr Leu Pro Leu Asp Pro Ala Ala Pro Glu Glu Arg Leu Ala
1640 1645 1650

His Ile Leu Asp Asp Ser Gly Val Arg Leu Leu Leu Thr Gln Gly
1655 1660 1665

His Leu Leu Glu Arg Leu Pro Arg Gln Ala Gly Val Glu Val Leu
1670 1675 1680

Ala Ile Asp Gly Leu Val Leu Asp Gly Tyr Ala Glu Ser Asp Pro
1685 1690 1695

Leu Pro Thr Leu Ser Ala Asp Asn Leu Ala Tyr Val Ile Tyr Thr
1700 1705 1710

Ser Gly Ser Thr Gly Lys Pro Lys Gly Thr Leu Leu Thr His Arg
1715 1720 1725

Asn Ala Leu Arg Leu Phe Ser Ala Thr Glu Ala Trp Phe Gly Phe
1730 1735 1740

Asp Glu Arg Asp Val Trp Thr Leu Phe His Ser Tyr Ala Phe Asp
1745 1750 1755

Phe Ser Val Trp Glu Ile Phe Gly Ala Leu Leu Tyr Gly Gly Arg

1760 1765 1770

Leu Val Ile Val Pro Gln Trp Val Ser Arg Ser Pro Glu Asp Phe
1775 1780 1785

Tyr Arg Leu Leu Cys Arg Glu Gly Val Thr Val Leu Asn Gln Thr
1790 1795 1800

Pro Ser Ala Phe Lys Gln Leu Met Ala Val Ala Cys Ser Ala Asp
1805 1810 1815

Met Ala Thr Gln Gln Pro Ala Leu Arg Tyr Val Ile Phe Gly Gly
1820 1825 1830

Glu Ala Leu Asp Leu Gln Ser Leu Arg Pro Trp Phe Gln Arg Phe
1835 1840 1845

Gly Asp Arg Gln Pro Gln Leu Val Asn Met Tyr Gly Ile Thr Glu
1850 1855 1860

Thr Thr Val His Val Thr Tyr Arg Pro Val Ser Glu Ala Asp Leu
1865 1870 1875

Lys Gly Gly Leu Val Ser Pro Ile Gly Gly Thr Ile Pro Asp Leu
1880 1885 1890

Ser Trp Tyr Ile Leu Asp Arg Asp Leu Asn Pro Val Pro Arg Gly
1895 1900 1905

Ala Val Gly Glu Leu Tyr Ile Gly Arg Ala Gly Leu Ala Arg Gly
1910 1915 1920

Tyr Leu Arg Arg Pro Gly Leu Ser Ala Thr Arg Phe Val Pro Asn
1925 1930 1935

Pro Phe Pro Gly Gly Ala Gly Glu Arg Leu Tyr Arg Thr Gly Asp
1940 1945 1950

Leu Ala Arg Phe Gln Ala Asp Gly Asn Ile Glu Tyr Ile Gly Arg
1955 1960 1965

Ile Asp His Gln Val Lys Val Arg Gly Phe Arg Ile Glu Leu Gly
1970 1975 1980

Glu Ile Glu Ala Ala Leu Ala Gly Leu Ala Gly Val Arg Asp Ala
1985 1990 1995

Val Val Leu Ala His Asp Gly Val Gly Gly Thr Gln Leu Val Gly

2000 2005 2010

Tyr Val Val Ala Asp Ser Ala Glu Asp Ala Glu Arg Leu Arg Glu
2015 2020 2025

Ser Leu Arg Glu Ser Leu Lys Arg His Leu Pro Asp Tyr Met Val
2030 2035 2040

Pro Ala His Leu Met Leu Leu Glu Arg Met Pro Leu Thr Val Asn
2045 2050 2055

Gly Lys Leu Asp Arg Gln Ala Leu Pro Gln Pro Asp Ala Ser Leu
2060 2065 2070

Ser Gln Gln Ala Tyr Arg Ala Pro Gly Ser Glu Leu Glu Gln Arg
2075 2080 2085

Ile Ala Ala Ile Trp Ala Glu Ile Leu Gly Val Glu Arg Val Gly
2090 2095 2100

Leu Asp Asp Asn Phe Phe Glu Leu Gly Gly His Ser Leu Leu Leu
2105 2110 2115

Leu Met Leu Lys Glu Arg Ile Gly Asp Thr Cys Gln Ala Thr Leu
2120 2125 2130

Ser Ile Ser Gln Leu Met Thr His Ala Ser Val Ala Glu Gln Ala
2135 2140 2145

Ala Cys Ile Glu Gly Gln Ala Arg Glu Ser Leu Leu Val Pro Leu
2150 2155 2160

Asn Gly Arg Arg Glu Gly Ser Pro Leu Phe Met Phe His Pro Ser
2165 2170 2175

Phe Gly Ser Val His Cys Tyr Lys Thr Leu Ala Met Ala Leu Arg
2180 2185 2190

Asp Arg His Pro Val Lys Gly Val Val Cys Arg Ala Leu Leu Gly
2195 2200 2205

Ala Gly Arg Glu Val Pro Glu Trp Asp Asp Met Val Ala Glu Tyr
2210 2215 2220

Ala Glu Gln Leu Leu Gln Glu His Pro Glu Gly Val Phe Asn Leu
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Ala Gly Trp Ser Leu Gly Gly Asn Leu Ala Met Asp Val Ala Ala

2240 2245 2250

Arg Leu Glu Gln Arg Gly Arg Gln Val Ala Phe Val Gly Trp Ile
2255 2260 2265

Asp Ala Pro Ala Pro Val Arg Val Glu Ala Phe Trp Asn Glu Ile
2270 2275 2280

Gly Pro Thr Pro Glu Ala Val Pro Asn Leu Ser Val Gly Glu Met
2285 2290 2295

Arg Val Glu Leu Leu Gly Val Met Phe Pro Glu Arg Ala Glu His
2300 2305 2310

Ile Glu Arg Ala Trp Ser Ser Ile Cys Ser Ala Thr Thr Asp Asp
2315 2320 2325

Glu Gln Arg Trp Thr Arg Met Ser Asp Trp Ala Glu Ala Glu Ile
2330 2335 2340

Gly Ala Glu Phe Ala Thr Leu Arg Ser Glu Ile Ala Gln Ser Asn
2345 2350 2355

Glu Leu Glu Val Ser Trp Glu Leu Lys Gln Ile Leu Asp Glu Arg
2360 2365 2370

Leu Lys Ala Met Asp Tyr Pro Arg Leu Thr Ala Lys Val Ser Leu
2375 2380 2385

Trp Trp Ala Ala Arg Ser Thr Asn Ala Ile Gln Arg Ser Ala Val
2390 2395 2400

Glu Arg Ser Met Ala Glu Ala Ile Gly Ala Glu Arg Val Glu Pro
2405 2410 2415

Val Arg Val Leu Asp Thr Arg His Asp Lys Ile Ile Asp His Pro
2420 2425 2430

Glu Phe Val Gln Ser Phe Arg Ala Ala Leu Glu Arg Ala Gly Arg
2435 2440 2445

<210> 19
<211> 3132
<212> DNA
<213> Pseudomonas aeruginosa

<400> 19
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accatcagcg gcacgctgtc cgctgccttc ggctcggagg tgatcaacga cttcaccaat 2280

gcggggcgcc aacagcgggt ggtgatccag gccgaacagg gcaaccggat gaccccggaa 2340

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gagcgcctgg cctcgcagct gccggccggc atcggctacg agtggaccgg cctgtcctat 2580

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gccggggagt ga 3132

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<211> 1043
<212> PRT
<213> Pseudomonas aeruginosa

<400> 20

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Ala Gln Tyr Pro Asn Val Ala Pro Pro Gln Ile Thr Ile Thr Ala Thr
35 40 45

Tyr Pro Gly Ala Ser Ala Lys Val Leu Val Asp Ser Val Thr Ser Val
50 55 60

Leu Glu Glu Ser Leu Asn Gly Ala Lys Gly Leu Leu Tyr Phe Glu Ser

65 70 75 80

Thr Asn Asn Ser Asn Gly Thr Ala Glu Ile Val Val Thr Phe Glu Pro
85 90 95

Gly Thr Asp Pro Asp Leu Ala Gln Val Asp Val Gln Asn Arg Leu Lys
100 105 110

Lys Ala Glu Ala Arg Met Pro Gln Ala Val Leu Thr Gln Gly Leu Gln
115 120 125

Val Glu Gln Thr Ser Ala Gly Phe Leu Leu Ile Tyr Ala Leu Ser Tyr
130 135 140

Lys Glu Gly Ala Gln Arg Ser Asp Thr Thr Ala Leu Gly Asp Tyr Ala
145 150 155 160

Ala Arg Asn Ile Asn Asn Glu Leu Arg Arg Leu Pro Gly Val Gly Lys
165 170 175

Leu Gln Phe Phe Ser Ser Glu Ala Ala Met Arg Val Trp Ile Asp Pro
180 185 190

Gln Lys Leu Val Gly Phe Gly Leu Ser Ile Asp Asp Val Ser Asn Ala
195 200 205

Ile Arg Gly Gln Asn Val Gln Val Pro Ala Gly Ala Phe Gly Ser Ala
210 215 220

Pro Gly Ser Ser Ala Gln Glu Leu Thr Ala Thr Leu Ala Val Lys Gly
225 230 235 240

Thr Leu Asp Asp Pro Gln Glu Phe Gly Gln Val Val Leu Arg Ala Asn
245 250 255

Glu Asp Gly Ser Leu Val Arg Leu Ala Asp Val Ala Arg Leu Glu Leu
260 265 270

Gly Lys Glu Ser Tyr Asn Ile Ser Ser Arg Leu Asn Gly Thr Pro Thr
275 280 285

Val Gly Gly Ala Ile Gln Leu Ser Pro Gly Ala Asn Ala Ile Gln Thr
290 295 300

Ala Thr Leu Val Lys Gln Arg Leu Ala Glu Leu Ser Ala Phe Phe Pro
305 310 315 320

Glu Asp Met Gln Tyr Ser Val Pro Tyr Asp Thr Ser Arg Phe Val Asp

325 330 335

Val Ala Ile Glu Lys Val Ile His Thr Leu Ile Glu Ala Met Val Leu
340 345 350

Val Phe Leu Val Met Phe Leu Phe Leu Gln Asn Val Arg Tyr Thr Leu
355 360 365

Ile Pro Ser Ile Val Val Pro Val Cys Leu Leu Gly Thr Leu Met Val
370 375 380

Met Tyr Leu Leu Gly Phe Ser Val Asn Met Met Thr Met Phe Gly Met
385 390 395 400

Val Leu Ala Ile Gly Ile Leu Val Asp Asp Ala Ile Val Val Val Glu
405 410 415

Asn Val Glu Arg Ile Met Ala Glu Glu Gly Ile Ser Pro Ala Glu Ala
420 425 430

Thr Val Lys Ala Met Lys Gln Val Ser Gly Ala Ile Val Gly Ile Thr
435 440 445

Leu Val Leu Ser Ala Val Phe Leu Pro Leu Ala Phe Met Ala Gly Ser
450 455 460

Val Gly Val Ile Tyr Gln Gln Phe Ser Val Ser Leu Ala Val Ser Ile
465 470 475 480

Leu Phe Ser Gly Phe Leu Ala Leu Thr Phe Thr Pro Ala Leu Cys Ala
485 490 495

Thr Leu Leu Lys Pro Ile Pro Glu Gly His His Glu Lys Arg Gly Phe
500 505 510

Phe Gly Ala Phe Asn Arg Gly Phe Ala Arg Val Thr Glu Arg Tyr Ser
515 520 525

Leu Leu Asn Ser Lys Leu Val Ala Arg Ala Gly Arg Phe Met Leu Val
530 535 540

Tyr Ala Gly Leu Val Ala Met Leu Gly Tyr Phe Tyr Leu Arg Leu Pro
545 550 555 560

Glu Ala Phe Val Pro Ala Glu Asp Leu Gly Tyr Met Val Val Asp Val
565 570 575

Gln Leu Pro Pro Gly Ala Ser Arg Val Arg Thr Asp Ala Thr Gly Glu

580 585 590

Glu Leu Glu Arg Phe Leu Lys Ser Arg Glu Ala Val Ala Ser Val Phe
595 600 605

Leu Ile Ser Gly Phe Ser Phe Ser Gly Gln Gly Asp Asn Ala Ala Leu
610 615 620

Ala Phe Pro Thr Phe Lys Asp Trp Ser Glu Arg Gly Ala Glu Gln Ser
625 630 635 640

Ala Ala Ala Glu Ile Ala Ala Leu Asn Glu His Phe Ala Leu Pro Asp
645 650 655

Asp Gly Thr Val Met Ala Val Ser Pro Pro Pro Ile Asn Gly Leu Gly
660 665 670

Asn Ser Gly Gly Phe Ala Leu Arg Leu Met Asp Arg Ser Gly Val Gly
675 680 685

Arg Glu Ala Leu Leu Gln Ala Arg Asp Thr Leu Leu Gly Glu Ile Gln
690 695 700

Thr Asn Pro Lys Phe Leu Tyr Ala Met Met Glu Gly Leu Ala Glu Ala
705 710 715 720

Pro Gln Leu Arg Leu Leu Ile Asp Arg Glu Lys Ala Arg Ala Leu Gly
725 730 735

Val Ser Phe Glu Thr Ile Ser Gly Thr Leu Ser Ala Ala Phe Gly Ser
740 745 750

Glu Val Ile Asn Asp Phe Thr Asn Ala Gly Arg Gln Gln Arg Val Val
755 760 765

Ile Gln Ala Glu Gln Gly Asn Arg Met Thr Pro Glu Ser Val Leu Glu
770 775 780

Leu Tyr Val Pro Asn Ala Ala Gly Asn Leu Val Pro Leu Ser Ala Phe
785 790 795 800

Val Ser Val Lys Trp Glu Glu Gly Pro Val Gln Leu Val Arg Tyr Asn
805 810 815

Gly Tyr Pro Ser Ile Arg Ile Val Gly Asp Ala Ala Pro Gly Phe Ser
820 825 830

Thr Gly Glu Ala Met Ala Glu Met Glu Arg Leu Ala Ser Gln Leu Pro

835 840 845

Ala Gly Ile Gly Tyr Glu Trp Thr Gly Leu Ser Tyr Gln Glu Lys Val
850 855 860

Ser Ala Gly Gln Ala Thr Ser Leu Phe Ala Leu Ala Ile Leu Val Val
865 870 875 880

Phe Leu Leu Leu Val Ala Leu Tyr Glu Ser Trp Ser Ile Pro Leu Ser
885 890 895

Val Met Leu Ile Val Pro Ile Gly Ala Ile Gly Ala Val Leu Ala Val
900 905 910

Met Val Ser Gly Met Ser Asn Asp Val Tyr Phe Lys Val Gly Leu Ile
915 920 925

Thr Ile Ile Gly Leu Ser Ala Lys Asn Ala Ile Leu Ile Val Glu Phe
930 935 940

Ala Lys Glu Leu Trp Glu Gln Gly His Ser Leu Arg Asp Ala Ala Ile
945 950 955 960

Glu Ala Ala Arg Leu Arg Phe Arg Pro Ile Ile Met Thr Ser Met Ala
965 970 975

Phe Ile Leu Gly Val Ile Pro Leu Ala Leu Ala Ser Gly Ala Gly Ala
980 985 990

Ala Ser Gln Arg Ala Ile Gly Thr Gly Val Ile Gly Gly Met Leu Ser
995 1000 1005

Ala Thr Phe Leu Gly Val Leu Phe Val Pro Ile Cys Phe Val Trp
1010 1015 1020

Leu Leu Ser Leu Leu Arg Ser Lys Pro Ala Pro Ile Glu Gln Ala
1025 1030 1035

Ala Ser Ala Gly Glu
1040

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<211> 642
<212> DNA
<213> Pseudomonas aeruginosa

<400> 21
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atagaacggg ccggtggttc acgggggacc ctgtacagct ccttcggcgg caaggagggc 180

ctgttcgccg cggtgatcgc ccacatgatc ggggaaatct tcgacgacag cgccgatcag 240

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<210> 22
<211> 213
<212> PRT
<213> Pseudomonas aeruginosa

<400> 22

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Arg Ala Met Leu Asp Ala Ala Thr Gln Ala Phe Leu Glu His Gly Phe
20 25 30

Glu Gly Thr Thr Leu Asp Met Val Ile Glu Arg Ala Gly Gly Ser Arg
35 40 45

Gly Thr Leu Tyr Ser Ser Phe Gly Gly Lys Glu Gly Leu Phe Ala Ala
50 55 60

Val Ile Ala His Met Ile Gly Glu Ile Phe Asp Asp Ser Ala Asp Gln
65 70 75 80

Pro Arg Pro Ala Ala Thr Leu Ser Ala Thr Leu Glu His Phe Gly Arg
85 90 95

Arg Phe Leu Thr Ser Leu Leu Asp Pro Arg Cys Gln Ser Leu Tyr Arg
100 105 110

Leu Val Val Ala Glu Ser Pro Arg Phe Pro Ala Ile Gly Lys Ser Phe
115 120 125

Tyr Glu Gln Gly Pro Gln Gln Ser Tyr Leu Leu Leu Ser Glu Arg Leu
130 135 140

Ala Ala Val Ala Pro His Met Asp Glu Glu Thr Leu Tyr Ala Val Ala

145 150 155 160

Cys Gln Phe Leu Glu Met Leu Lys Ala Asp Leu Phe Leu Lys Ala Leu
165 170 175

Ser Val Ala Asp Phe Gln Pro Thr Met Ala Leu Leu Glu Thr Arg Leu
180 185 190

Lys Leu Ser Val Asp Ile Ile Ala Cys Tyr Leu Glu His Leu Ser Gln
195 200 205

Ser Pro Ala Gln Gly
210

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<211> 1017
<212> DNA
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<211> 338
<212> PRT
<213> Pseudomonas aeruginosa

<400> 24

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Cys Leu Pro Glu Leu Phe Val Ala Glu Gly Trp Gly Glu Val Pro Pro
20 25 30

Ala Glu Leu Ile Pro Ala Ser Ser Asp Ala Ser Phe Arg Arg Tyr Phe
35 40 45

Arg Trp Gln Gly Gly Asp Arg Ser Leu Val Val Met Asp Ala Pro Pro
50 55 60

Pro Gln Glu Asp Cys Arg Pro Phe Val Lys Val Ala Gly Leu Leu Ala
65 70 75 80

Gly Ala Gly Val His Val Pro Arg Ile Leu Ala Gln Asp Leu Glu Asn
85 90 95

Gly Phe Leu Leu Leu Ser Asp Leu Gly Arg Gln Thr Tyr Leu Asp Val
100 105 110

Leu His Pro Gly Asn Ala Asp Glu Leu Phe Glu Pro Ala Leu Asp Ala
115 120 125

Leu Ile Ala Phe Gln Lys Val Asp Val Ala Gly Val Leu Pro Ala Tyr
130 135 140

Asp Glu Ala Val Leu Arg Arg Glu Leu Gln Leu Phe Pro Asp Trp Tyr
145 150 155 160

Leu Ala Arg His Leu Gly Val Glu Leu Glu Gly Glu Thr Leu Ala Arg
165 170 175

Trp Lys Arg Ile Cys Asp Leu Leu Val Arg Ser Ala Leu Glu Gln Pro
180 185 190

Arg Val Phe Val His Arg Asp Tyr Met Pro Arg Asn Leu Met Leu Ser
195 200 205

Glu Pro Asn Pro Gly Val Leu Asp Phe Gln Asp Ala Leu His Gly Pro
210 215 220

Val Thr Tyr Asp Val Thr Cys Leu Tyr Lys Asp Ala Phe Val Ser Trp
225 230 235 240

Pro Glu Pro Arg Val His Ala Ala Leu Asn Arg Tyr Trp Lys Lys Ala

245 250 255

Thr Trp Ala Gly Ile Pro Leu Pro Pro Ser Phe Glu Asp Phe Leu Arg
260 265 270

Ala Ser Asp Leu Met Gly Val Gln Arg His Leu Lys Val Ile Gly Ile
275 280 285

Phe Ala Arg Ile Cys His Arg Asp Gly Lys Pro Arg Tyr Leu Gly Asp
290 295 300

Val Pro Arg Phe Phe Arg Tyr Leu Glu Thr Ala Val Ala Arg Arg Pro
305 310 315 320

Glu Leu Ala Glu Leu Gly Glu Leu Leu Ala Ser Leu Pro Gln Gly Ala
325 330 335

Glu Ala

<210> 25
<211> 3270
<212> DNA
<213> Pseudomonas aeruginosa

<400> 25
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gtgccggtgc tggtcaaggg gcagttcgtg atcccacgct acaccatggc ctatagcgaa 480

actccctggc cttggtcgta catcgactgg ctggaggagg acccgcagcg ggtcaaccgg 540

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<213> Pseudomonas aeruginosa

<400> 26

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35 40 45

Gly His Glu Glu His Glu Arg Ile Gln Gln Asn Thr Phe Leu Ala Val
50 55 60

Met Pro Leu Val Arg Leu Pro Thr Leu Gly Lys Ala Gly Tyr Gly Asp
65 70 75 80

Gln Leu Pro Ala Gly Ala Leu Pro Arg Ala Gly Arg Ile Tyr Leu Phe
85 90 95

Gln Asp Gly Lys Leu Trp Arg Glu Leu Glu Cys Asp Gly Lys Gly Asn
100 105 110

Leu Phe Glu Val Asp Leu Leu Gln Gly Arg Ser Gln Arg Ala Asp Lys
115 120 125

Arg Pro Ala Leu Gly Lys Thr Gln Ala Leu Ile Leu Val Pro Val Leu
130 135 140

Val Lys Gly Gln Phe Val Ile Pro Arg Tyr Thr Met Ala Tyr Ser Glu
145 150 155 160

Thr Pro Trp Pro Trp Ser Tyr Ile Asp Trp Leu Glu Glu Asp Pro Gln

165 170 175

Arg Val Asn Arg Arg Cys Gln Gln Met Ala Ser Ala Trp Asn Ala Ser
180 185 190

Val Ala Asn Gln His Trp Lys Ala Ser Ile His Gln Pro Ala Leu Val
195 200 205

Ile Asp His His Ala Gln Gly Leu Arg Pro Arg Asp Phe Asn Val Glu
210 215 220

Ser Ala Leu Glu Asp Pro Ala Glu Phe Thr Pro Glu Phe Ala Ala Phe
225 230 235 240

Arg Glu Glu Ser Leu Val Cys Gln Leu Gln Arg Arg Gln Gln Glu Leu
245 250 255

Ala Pro Leu Leu Lys Gln Ala Pro Pro Ser Ala Leu Pro Thr Leu Glu
260 265 270

Ala Gly Glu Asp Val Leu Glu Thr Leu Lys Leu Arg Gly His Pro Asn
275 280 285

Leu Ile Gly Leu Met Leu Asp Asp Ser Leu Phe Ala Leu Arg His Ala
290 295 300

Ala Ala Gln Ala Arg His Cys Ala Ala Tyr Leu Arg Ser Leu Asn Ala
305 310 315 320

Leu Leu Pro His Arg Pro Asn Gly Arg Tyr Ala Gln Val Leu Ser Asn
325 330 335

Met Leu Asp Gly Pro Leu Ala Lys Leu Arg Gly Glu Val Asp Gln Ala
340 345 350

Glu Leu Asp Glu Ala Ile Phe Ala Glu Glu Arg Gln Ser Cys Arg Ile
355 360 365

His Leu Thr Gln Gln Val Glu His Leu Val Ala Leu Leu Glu Gly Pro
370 375 380

Leu His Pro Val Leu Gln Asp Trp Thr His Gln Cys Asp Glu Ala Leu
385 390 395 400

Leu Glu Pro Tyr Ser Leu Met Ser Glu Ala Leu Ala Ala Leu Asn Gln
405 410 415

Leu Pro Asp Arg Cys Asp Ala Leu Tyr Ser Gly Thr Ala Tyr Arg Ala

420 425 430

Leu Ala Ala His Val Glu Arg Val Val Ser Thr Val Leu Gln Ala Ser
435 440 445

His Pro Leu Gly Ala Met Leu Leu Ala Lys Asp Glu Gly Gln Leu Pro
450 455 460

Glu Pro Val Arg Arg Leu Gln Ala Leu Arg Asp Ser Pro Arg Thr Pro
465 470 475 480

Asp Pro Asp Ala Met Gly Leu Ser Thr Leu Met Leu Gly Ala Ser Leu
485 490 495

Leu Gly Glu Val Asp Gln Pro Ser Ala Gly Lys Ser Leu Ala Tyr Phe
500 505 510

Leu Gly Asp Leu Leu Asp Val Phe Gly Ala Ser Val Val Glu Gln Leu
515 520 525

Gly Arg Leu Ser Gln Gly Ala Thr Gln Ile Gln Leu Asp Arg Leu Phe
530 535 540

Ala Pro Thr Phe Asn Thr Leu Ser Ala Leu Ser Val Lys Met Lys Gly
545 550 555 560

Ile Arg Leu Leu Pro Asp Ser Gln Val Pro Leu Asp Met Val Val Val
565 570 575

Gly Val Arg Gly Ala Gly Leu Arg Asn Gly Leu Thr Glu Val Glu Arg
580 585 590

Gln Glu Leu Arg Arg Lys Ser Tyr Arg Arg Ala Ile Val Gln Asp Gly
595 600 605

Ala Gly Asn Pro Leu Ala Gly Thr Ser Pro Arg Asp Thr Gly Met Ser
610 615 620

Arg Ala Asn Leu Arg Asn Val Met Val Val Ala Val Pro Lys Asp His
625 630 635 640

Pro Asp Leu Leu Ala Tyr Thr Lys Phe Arg Thr Gln Leu Gly Thr Leu
645 650 655

Thr Gln Val Met Glu Asn Thr Arg Ile Val Pro Thr Met Met Leu Gly
660 665 670

Phe Ala Ile Tyr Asn Leu Asn Val Gln Val Gln Ala Tyr Ser Gly Phe

675 680 685

Val Asp Ser Gly Glu Lys His Arg Gly Thr Ile Gly Ala Val Gly Ala
690 695 700

Val Ile Asp Leu Thr Ala Ala Gly Gly Ser His Ala Lys Leu Leu Phe
705 710 715 720

Gly Pro Ser Thr Ala Lys Tyr Leu Glu Thr Pro Arg Ile Ser Val Ala
725 730 735

Gln Ile Ser Pro Arg Trp Ala Arg Asn Leu Glu Val Gln Thr Gly Ser
740 745 750

Pro Lys Leu Gly Leu Leu Arg Gly Leu Gly Gly Ala Ala Thr Leu Phe
755 760 765

Gly Ala Gly Ile Ser Val Trp Asp Gly Tyr Arg Ala Leu Arg Gln Gly
770 775 780

Asp Ser Asp Ala Ala Ala Ala Tyr Gly Val Ala Ala Val Gly Gly Gly
785 790 795 800

Leu Trp Gly Ala Tyr Val Leu Gly Trp Ile Val Asn Pro Tyr Ala Leu
805 810 815

Leu Ala Gly Ala Val Leu Ala Ile Gly Gly Thr Val Val Ala Asn Leu
820 825 830

Leu Thr Asp Ser Asp Ala Glu Thr Ile Val Lys Lys Gly Pro Phe Gly
835 840 845

Arg Gln Phe Ala Glu Ala Gly Leu Leu Asp Ser Leu Met Gly Gln Asp
850 855 860

Gln Arg Phe Ala His Leu Lys Asp Pro Gln Thr Ala Tyr Arg Gln Leu
865 870 875 880

Leu Gly Val Leu Gly His Pro Arg Val Phe Val His Arg Leu Glu Asp
885 890 895

Trp Arg Lys Leu Ala Pro Ala Ala His Arg Ser Val Leu Gln Glu Ala
900 905 910

Glu Arg Gly Arg Gln Ala Val Ser Arg Thr Ala Leu Ser Cys Ile Asp
915 920 925

Pro Lys Leu Gln Ala Leu Glu Ala Asn Asp Trp Ala Val Val Leu Ser

930 935 940

Ser Pro Leu Leu Ala Met Phe Glu Asn Gly Gln Lys Ala Phe Arg Leu
945 950 955 960

Val Ala Gln Glu Phe Leu Ser Ser Leu Pro Ile Asp Pro Gly Thr Leu
965 970 975

Phe Gly Val Lys Arg Tyr His Arg Val Pro Ala Gly Pro Ala Lys Leu
980 985 990

Glu Ala Leu Pro Leu Asp Ala Ala Ser Val Leu Tyr Val Leu Pro Ala
995 1000 1005

Ser Leu Pro Ile Pro Gln Leu Ser Pro Arg Ala Arg Tyr Ser Met
1010 1015 1020

Arg Met Thr Gln Gly Leu Lys Ile Ser Ala Gln Phe Glu Leu Asn
1025 1030 1035

Ala Asp Gln Pro Glu Gln Arg Leu Val Leu Pro Gln Pro Ser Pro
1040 1045 1050

Lys Ser Trp Ser Ala Phe Thr Ser Ala Asn Arg Tyr Leu Pro Pro
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Asn Ser Glu Phe Asn Val
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<212> DNA
<213> Pseudomonas aeruginosa

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ccggccaccc gcctggagga cctcgccgac ggcgccgccc tcgccctgcg cgatttcgcc 240

gacgcgcccc tggcgctgtt cggccacagt ctcggcgcgg cgctggccta cgaaaccgcc 300

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<213> Pseudomonas aeruginosa

<400> 28

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35 40 45

Gln Tyr Pro Gly Arg Glu Asp Arg Phe Asn Glu Ala Pro Ala Thr Arg
50 55 60

Leu Glu Asp Leu Ala Asp Gly Ala Ala Leu Ala Leu Arg Asp Phe Ala
65 70 75 80

Asp Ala Pro Leu Ala Leu Phe Gly His Ser Leu Gly Ala Ala Leu Ala
85 90 95

Tyr Glu Thr Ala Leu Arg Leu Glu Ser Ala Gly Ala Pro Leu Arg His
100 105 110

Leu Phe Val Ser Ala His Pro Ala Pro His Arg Gln Arg Gly Gly Ala
115 120 125

Leu His Arg Gly Asp Glu Ala Ala Leu Leu Glu Asp Val Arg Arg Gln
130 135 140

Gly Gly Ala Ser Glu Leu Leu Glu Asp Ala Asp Leu Arg Ala Leu Phe
145 150 155 160

Leu Pro Ile Leu Arg Ala Asp Tyr Gln Ala Ile Glu Thr Tyr Arg Arg
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Ala Gln Pro Ile Ala Leu Ala Cys Ala Leu Asp Val Leu Leu Gly Glu

180 185 190

His Asp Glu Glu Val Ser Ala Ala Glu Ala Gln Ala Trp Ser Asp Ala
195 200 205

Ser Arg Thr Pro Ala Arg Leu Arg Arg Phe Pro Gly Gly His Phe Tyr
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Ala His Pro Asp Ala Leu Ser Arg Glu Val Ala
245 250

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<211> 4317
<212> DNA
<213> Pseudomonas aeruginosa

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<212> PRT
<213> Pseudomonas aeruginosa

<400> 30

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35 40 45

Leu Met Tyr Leu Gln Glu Arg Leu Arg Ala Arg Gly Ser Thr Leu Asp
50 55 60

Phe Ala Gln Leu Ala Gln Arg Pro Cys Leu Gly Ala Trp Leu Asp Leu
65 70 75 80

Leu Ala Cys Ala Asp Arg Leu Ser Ala Pro Ala Thr Val Ala Leu Pro
85 90 95

Thr Ala Gln Asp Arg Asp Gln Pro Phe Glu Leu Ser Ser Val Gln Gln
100 105 110

Ala Tyr Trp Leu Gly Arg Gly Ala Gly Glu Val Leu Gly Asn Val Ser
115 120 125

Cys His Ala Phe Leu Glu Phe Arg Thr Arg Asp Val Asp Pro Gln Arg
130 135 140

Leu Ala Ala Ala Ala Glu Cys Val Arg Gln Arg His Pro Met Leu Arg
145 150 155 160

Ala Arg Phe Leu Asp Gly Arg Gln Gln Ile Leu Pro Thr Pro Pro Leu
165 170 175

Ser Cys Phe Asp Leu Gln Asp Trp Arg Thr Leu Gln Val Asp Glu Ala
180 185 190

Glu Arg Asp Trp Gln Ala Leu Arg Asp Trp Arg Ala His Glu Cys Leu
195 200 205

Ala Val Glu Arg Gly Gln Val Phe Leu Leu Gly Leu Val Arg Met Pro
210 215 220

Gly Gly Glu Asp Arg Leu Trp Leu Ser Leu Asp Leu Leu Ala Ala Asp
225 230 235 240

Val Glu Ser Leu Arg Leu Leu Leu Ala Glu Leu Gly Val Ala Tyr Leu
245 250 255

Ala Pro Glu Arg Leu Ala Glu Pro Pro Ala Leu His Phe Ala Asp Tyr
260 265 270

Leu Ala His Arg Ala Ala Gln Arg Ala Glu Ala Ala Ala Arg Ala Arg
275 280 285

Asp Tyr Trp Leu Glu Arg Leu Pro Arg Leu Pro Asp Ala Pro Ala Leu
290 295 300

Pro Leu Ala Cys Ala Pro Glu Ser Ile Arg Gln Pro Arg Thr Arg Arg
305 310 315 320

Leu Ala Phe Gln Leu Ser Ala Gly Glu Ser Arg Arg Leu Glu Arg Leu
325 330 335

Ala Ala Gln His Gly Val Thr Leu Ser Ser Val Phe Gly Cys Ala Phe
340 345 350

Ala Leu Val Leu Ala Arg Trp Ser Glu Ser Ala Glu Phe Leu Leu Asn
355 360 365

Val Pro Leu Phe Asp Arg His Ala Asp Asp Pro Arg Ile Gly Glu Val
370 375 380

Ile Ala Asp Phe Thr Thr Leu Leu Leu Leu Glu Cys Arg Met Gln Ala
385 390 395 400

Gly Val Ser Phe Ala Glu Ala Val Lys Ser Phe Gln Arg Asn Leu His
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Gly Ala Ile Asp His Ala Ala Phe Pro Ala Leu Glu Val Leu Arg Glu
420 425 430

Ala Arg Arg Gln Gly Gln Pro Arg Ser Ala Pro Val Val Phe Ala Ser
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Asn Leu Gly Glu Glu Gly Phe Val Pro Ala Ala Phe Arg Asp Ala Phe
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Gly Asp Leu His Asp Met Leu Ser Gln Thr Pro Gln Val Trp Leu Asp
465 470 475 480

His Gln Leu Tyr Arg Val Gly Asp Gly Ile Leu Leu Ala Trp Asp Ser
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Val Val Gly Leu Phe Pro Glu Gly Leu Pro Glu Thr Met Phe Glu Ala
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Tyr Val Gly Leu Leu Gln Arg Leu Cys Asp Ser Ala Trp Gly Gln Pro
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Ala Asp Leu Pro Leu Pro Trp Ala Gln Gln Ala Arg Arg Ala Leu Leu
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Asn Gly Gln Pro Ala Cys Ala Thr Ala Arg Thr Leu His Arg Asp Phe
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Phe Leu Arg Ala Ala Glu Ala Pro Asp Ala Asp Ala Leu Leu Tyr Arg
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Asp Gln Arg Val Thr Arg Gly Glu Leu Ala Glu Arg Ala Leu Arg Ile
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Ala Gly Gly Leu Arg Glu Ala Gly Val Arg Pro Gly Asp Ala Val Glu
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Val Ser Leu Pro Arg Gly Pro Gln Gln Val Ala Ala Val Phe Gly Val
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Leu Ala Ala Gly Ala Cys Tyr Val Pro Leu Asp Ile Asp Gln Pro Pro
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Ala Arg Arg Arg Leu Ile Glu Glu Ala Ala Gly Val Cys Leu Ala Ile
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Thr Glu Glu Asp Asp Pro Gln Ala Leu Pro Pro Arg Leu Asp Val Gln
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Arg Leu Leu Arg Gly Pro Ala Leu Ala Ala Pro Val Pro Leu Ala Pro
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Gln Ala Ser Ala Tyr Val Ile Tyr Thr Ser Gly Ser Thr Gly Val Pro
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Lys Gly Val Glu Val Ser His Ala Ala Ala Ile Asn Thr Ile Asp Ala
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Leu Leu Asp Leu Leu Arg Val Asn Ala Ser Asp Arg Leu Leu Ala Val
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Ser Ala Leu Asp Phe Asp Leu Ser Val Phe Asp Leu Phe Gly Gly Leu
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Gly Ala Gly Ala Ser Leu Val Leu Pro Ala Gln Glu Gln Ala Arg Asp
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Ala Ala Ala Trp Ala Glu Ala Ile Gln Arg His Ala Val Ser Leu Trp
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Asn Ser Ala Pro Ala Leu Leu Glu Met Ala Leu Ser Leu Pro Ala Ser
785 790 795 800

Gln Ala Asp Tyr Arg Ser Leu Arg Ala Val Leu Leu Ser Gly Asp Trp
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Val Ala Leu Asp Leu Pro Gly Arg Leu Arg Pro Arg Cys Ala Glu Gly
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Cys Arg Leu His Val Leu Gly Gly Ala Thr Glu Ala Gly Ile Trp Ser
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Asn Leu Gln Ser Val Asp Thr Val Pro Pro His Trp Arg Ser Ile Pro
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Tyr Gly Arg Pro Leu Pro Gly Gln Ala Tyr Arg Val Val Asp Thr His
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Gly Arg Asp Val Pro Asp Leu Val Val Gly Glu Leu Trp Ile Gly Gly
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Ala Ser Leu Ala Arg Gly Tyr Arg Asn Asp Pro Glu Leu Ser Ala Arg
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Arg Phe Val His Asp Ala Gln Gly Arg Trp Tyr Arg Thr Gly Asp Arg
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Gly Arg Tyr Trp Gly Asp Gly Thr Leu Glu Phe Leu Gly Arg Val Asp
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Gln Gln Val Lys Val Arg Gly Gln Arg Ile Glu Leu Gly Glu Val Glu
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Ala Pro Arg Ala Glu Gly Ser Met Asp Leu Pro Ala Ala Gln Pro Phe
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Ala Gly Leu Ala Glu Ala Glu Ala Val Leu Thr Arg Glu Ile Leu
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Pro Ser Leu Asp Glu Ala Leu Arg Arg Leu Gly Trp Gln Ala Ala
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Gly Leu Thr Ala Met Gly Asn Ala Leu Arg Gly Leu Leu Ala Gly
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Glu His Leu Gly Arg Tyr Asp Arg Val Ile Ser Phe Ala Ala Leu
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Ala His Gln Arg Phe Pro Leu Thr Pro Val Gln Ala Ala Tyr Val Leu
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Gly Arg Gln Ala Ala Phe Asp Tyr Gly Gly Asn Ala Cys Gln Leu Tyr
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Ala Glu Tyr Asp Trp Pro Ala Asp Thr Asp Pro Ala Arg Leu Glu Ala
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Ala Trp Asn Ala Met Val Glu Arg His Pro Met Leu Arg Ala Val Ile
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Leu Thr Val His Ala Cys Ala Gly Leu Asp Glu Ala Ala Phe Gln Ala
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His Leu Glu Arg Val Arg Glu Arg Leu Asp His Ala Cys Ala Ala Leu
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Asp Gln Trp Pro Val Leu Arg Pro Glu Leu Ser Ile Gly Arg Asp Ala
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Cys Val Leu His Cys Ser Val Asp Phe Thr Leu Val Asp Tyr Ala Ser
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Arg Leu Asp Glu Ala Ala Trp Gln Ala Leu Gly Ala Arg Ala Gly Glu
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His Gly Leu Ser Ala Ala Gly Val Ala Leu Ala Ala Phe Ala Glu Thr
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Leu Asn Arg Pro Pro Leu His Pro Gln Leu Ala Gln Val Leu Gly Asp
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Phe Thr Ala Leu Ser Leu Leu Ala Val Asp Ser Arg His Gly Asp Ser
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Phe Val Glu Arg Ala Arg Arg Ile Gly Glu Gln Met Phe Asp Asp Leu
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Asp His Pro Thr Phe Ser Gly Val Asp Leu Leu Arg Glu Leu Ala Arg
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Cys Ala His Pro Gln Val Asn Leu Ala Ala Thr Val Val Leu Gly Glu
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Thr His Glu Arg Ser Leu Ala Ser Phe Val Thr Leu His Ala Pro Val
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Glu Ala Gly Glu Asp Pro Arg Thr Ala Leu Asp Ala Val Arg Gln Arg
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Gly Leu Val Ala Leu Glu Thr Ala Lys Ser Leu Val Gln Arg Gly
1610 1615 1620

Val Arg Val Arg Gln Leu Asp Ile Val Ser Ser Tyr Arg Ile Pro
1625 1630 1635

Tyr Arg Val Asp Asp Glu Arg Leu Leu Leu Phe Ser Phe Ala Ala
1640 1645 1650

Thr Leu Gly Leu Asp Thr Ala Ala Leu Gly Phe Pro Ala Pro Glu
1655 1660 1665

Arg Leu Gly Gln Ala Val Gln Ala Ala Leu Ala Gln Thr Pro Glu
1670 1675 1680

Arg Leu Val Ala Glu Ala Leu Ala Gly Leu Pro Gly Leu Ala Asp
1685 1690 1695

Leu Val Ala Leu Arg Gly Arg Val Leu Gln Ala Ala Ser Gly Ser
1700 1705 1710

Ala Asp Ala Val Ser Val Glu Arg Asp Thr Leu Tyr Arg Leu Phe
1715 1720 1725

Cys His Ser Val Arg Ala Ser Gln Ala Glu Ala Pro Glu Pro Tyr
1730 1735 1740

Val Gly Ala Leu Arg Leu Phe Val Pro Asp Ala Gly Asn Pro Leu
1745 1750 1755

Val Pro Arg Tyr Ala Glu Ala Leu Glu Thr Gln Trp Arg Ala Ala
1760 1765 1770

Ala Leu Gly Ala Cys Gly Ile His Glu Val Pro Gly Gly His Phe
1775 1780 1785

Asp Cys Leu Gly Glu Ala Leu Ala Gln Ser Leu Ser Lys Pro Met
1790 1795 1800

Pro Glu Glu Ala Ser Arg
1805

<210> 33
<211> 1713
<212> DNA
<213> Pseudomonas aeruginosa

<400> 33
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cgtgaacaga acggcgcgga ggtggcggca tga 1713

<210> 34
<211> 570
<212> PRT
<213> Pseudomonas aeruginosa

<400> 34

Met Thr Pro Val Leu Trp Arg Leu Leu Arg Thr Tyr Arg Trp Arg Leu
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Ala Ala Ala Met Gly Leu Gln Ala Leu Ala Gly Leu Cys Ser Leu Leu
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Pro Trp Met Leu Leu Ala Trp Leu Ala Glu Pro Leu Ala Arg Gly Gln
35 40 45

Ala Gln Pro Ala Leu Leu Ala Leu Val Leu Leu Ala Val Leu Ala Trp
50 55 60

Leu Gly Cys Gln Ala Leu Ala Ala His Leu Ala His Arg Val Asp Ala
65 70 75 80

Asp Leu Cys Asn Asp Leu Arg Leu Arg Leu Leu Ala His Leu Gln Arg
85 90 95

Leu Pro Leu Asp Trp Phe Gly Arg Gln Gly Pro Asp Gly Val Ala Arg
100 105 110

Leu Val Glu Gln Asp Val Arg Ala Leu His Gln Leu Ile Ala His Ala
115 120 125

Pro Asn Asp Leu Ser Asn Leu Leu Val Val Pro Leu Val Ala Leu Leu
130 135 140

Trp Leu Ala Trp Leu His Pro Trp Leu Leu Leu Phe Cys Leu Leu Pro
145 150 155 160

Leu Val Leu Ala Ala Ala Gly Phe Leu Leu Leu Arg Ser Ala Arg Tyr
165 170 175

Arg Asp Leu Val Leu Arg Arg Asn Ala Ala Leu Glu Arg Leu Ser Ala
180 185 190

Asp Tyr Gly Glu Phe Ala His Asn Leu Leu Leu Ala Arg Gln Tyr Pro
195 200 205

Gly Ala Gly Ile Gln Gln Gly Ala Glu Ala Ser Ala Ala Ala Phe Gly
210 215 220

Glu Ala Phe Gly Ala Trp Val Lys Arg Val Gly His Leu Ala Ala Leu
225 230 235 240

Val Tyr Val Gln Leu Ser Thr Pro Trp Leu Leu Ala Trp Val Leu Leu
245 250 255

Gly Ala Leu Ala Leu Asp Ala Leu Gly Val Pro Leu Ala Leu Gly Gln
260 265 270

Ala Cys Ala Phe Leu Leu Leu Leu Arg Ala Leu Ala Ala Pro Val Gln
275 280 285

Ala Leu Gly His Gly Gly Asp Ala Leu Leu Gly Ala Arg Ala Ala Ala
290 295 300

Glu Arg Leu Gln Gln Val Phe Asp Gln Ala Pro Leu Ala Glu Gly Arg
305 310 315 320

Ser Thr Arg Glu Pro Val Asp Gly Ala Val Ala Leu His Gly Leu Gly
325 330 335

His Ala Tyr Glu Gly Val Glu Val Leu Ala Asp Ile Asp Leu Glu Leu
340 345 350

Glu Asp Gly Ser Leu Val Ala Leu Val Gly Pro Ser Gly Ser Gly Lys
355 360 365

Ser Thr Leu Leu His Leu Leu Ala Arg Tyr Met Asp Ala Gln Arg Gly
370 375 380

Glu Leu Glu Val Gly Gly Leu Ala Leu Lys Asp Met Pro Asp Ala Val
385 390 395 400

Arg His Arg His Ile Ala Leu Val Gly Gln Gln Ala Ala Ala Leu Glu
405 410 415

Ile Ser Leu Ala Asp Asn Ile Ala Leu Phe Arg Pro Asp Ala Asp Leu
420 425 430

Gln Glu Ile Arg Gln Ala Ala Arg Asp Ala Cys Leu Asp Glu Arg Ile
435 440 445

Met Ala Leu Pro Arg Gly Tyr Asp Ser Val Pro Gly Arg Asp Leu Gln
450 455 460

Leu Ser Gly Gly Glu Leu Gln Arg Leu Ala Leu Ala Arg Ala Leu Leu
465 470 475 480

Ser Pro Ala Ser Leu Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp
485 490 495

Pro Gln Thr Ala Arg Gln Val Leu Arg Asn Leu Arg Glu Arg Gly Gly
500 505 510

Gly Arg Thr Arg Val Ile Val Ala His Arg Leu Ala Glu Val Ser Asp
515 520 525

Ala Asp Leu Ile Leu Val Leu Val Ala Gly Arg Leu Val Glu Arg Gly
530 535 540

Glu His Ala Ala Leu Leu Ala Ala Asp Gly Ala Tyr Ala Arg Leu Trp
545 550 555 560

Arg Glu Gln Asn Gly Ala Glu Val Ala Ala
565 570

<210> 35
<211> 1725
<212> DNA
<213> Pseudomonas aeruginosa

<400> 35
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ccgttggtcg aggcctggtt cgccgaaggc gcgttgccct ggcgctgggt cgccgcgttg 180

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ctcggggtga tcctcgggct gttcctgatc gacccgtcca tcgccctcgg cctgctcctt 480

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gatgcccggc tggccgccga gcgcgacgcc gcacggcagt tgcaggcgtt cgccgaacgc 600

cagccactgc tgcgcgcggc gcagcgcgaa agcgtcgccc gccaggggct ggaagaggcc 660

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ttcatcgagc cgctggccca gctcacccat ctcgaccagg cgttgcgcgg cgcctggcag 900

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gccgccagtc gtaacctggt gttccaggac aacggcctgt tccgcggcag cgttgcctgg 1260

aacctgcgca tggcgcgagc ggacgccgat ctcgaagcgc tgcgcgaggc ggcgcgggcg 1320

gttggcctgc tggaagagat cgaggcctgg ccgcagggct gggacagcga cgtcggtccc 1380

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caccgcccgg cgctggcgcg tcaggccgac caggtactgc tgctggagga ggggcgcctg 1620

cgcctcagcg gacttcacgc cgatctgctc gtccgggacg actggtatgc cggtttcgtc 1680

gggctggcgg gcgaggaaag ttccgcgacg gtcgtggatc gatag 1725

<210> 36
<211> 574
<212> PRT
<213> Pseudomonas aeruginosa

<400> 36

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Ala Ala Cys Gly Val Leu Leu Val Pro Leu Val Glu Ala Trp Phe Ala
35 40 45

Glu Gly Ala Leu Pro Trp Arg Trp Val Ala Ala Leu Leu Gly Leu Ser
50 55 60

Leu Ala Gln Ala Leu Leu Gln Tyr Leu Ala Leu Arg Arg Gly Phe Ala
65 70 75 80

Ala Gly Gly Ser Leu Ala Ala Gly Leu Val Arg Ser Leu Val Ala Arg
85 90 95

Leu Pro Arg Leu Ala Pro Pro Ala Leu Arg Arg Val Ala Pro Ala Glu
100 105 110

Gly Leu Leu Arg Gly Pro Val Met Gln Ala Met Gly Ile Pro Ala His
115 120 125

Leu Leu Gly Pro Leu Ile Ala Ala Leu Val Thr Pro Leu Gly Val Ile
130 135 140

Leu Gly Leu Phe Leu Ile Asp Pro Ser Ile Ala Leu Gly Leu Leu Leu
145 150 155 160

Ala Gly Ala Phe Leu Ala Ala Leu Leu Arg Trp Ser Gly Arg Arg Asn
165 170 175

Leu Ala Ala Glu Asp Ala Arg Leu Ala Ala Glu Arg Asp Ala Ala Arg
180 185 190

Gln Leu Gln Ala Phe Ala Glu Arg Gln Pro Leu Leu Arg Ala Ala Gln
195 200 205

Arg Glu Ser Val Ala Arg Gln Gly Leu Glu Glu Ala Leu Arg Ser Leu
210 215 220

His Arg Ser Thr Leu Asp Leu Leu Arg Arg Ser Leu Pro Ser Gly Leu
225 230 235 240

Gly Phe Ala Leu Ala Val Gln Ala Ala Phe Ala Phe Ala Leu Leu Gly
245 250 255

Gly Ala Trp Ala Val Glu Arg Gln Trp Leu Asp Gly Ala Arg Leu Val
260 265 270

Ala Val Leu Val Leu Leu Val Arg Phe Ile Glu Pro Leu Ala Gln Leu
275 280 285

Thr His Leu Asp Gln Ala Leu Arg Gly Ala Trp Gln Ala Leu Asp Thr
290 295 300

Leu Leu Arg Val Phe Ala Leu Ala Pro Leu Arg Ser Pro Glu Pro Gly
305 310 315 320

Glu Arg Pro His Asp Ala Ser Leu Ala Ala Glu Ala Val Glu Leu Arg
325 330 335

Leu Glu Asp Gly Arg Ala Leu Leu Glu Asp Ile Ser Leu Arg Leu Glu
340 345 350

Pro Gly Ser Leu Asn Val Leu Val Gly Pro Ser Gly Ala Gly Lys Ser
355 360 365

Ser Leu Leu Ala Leu Leu Gly Arg Leu Tyr Asp Val Asp Ala Gly Arg
370 375 380

Val Leu Leu Gly Gly Val Asp Ile Arg Arg Leu Ser Glu Thr Thr Leu
385 390 395 400

Ala Ala Ser Arg Asn Leu Val Phe Gln Asp Asn Gly Leu Phe Arg Gly
405 410 415

Ser Val Ala Trp Asn Leu Arg Met Ala Arg Ala Asp Ala Asp Leu Glu
420 425 430

Ala Leu Arg Glu Ala Ala Arg Ala Val Gly Leu Leu Glu Glu Ile Glu
435 440 445

Ala Trp Pro Gln Gly Trp Asp Ser Asp Val Gly Pro Gly Gly Ala Leu
450 455 460

Leu Ser Gly Gly Gln Arg Gln Arg Leu Cys Leu Ala Arg Gly Leu Leu
465 470 475 480

Ser Thr Ala Pro Leu Leu Leu Leu Asp Glu Pro Thr Ala Ser Leu Asp
485 490 495

Ala Ala Ser Glu Ala Gln Val Leu Arg Ser Leu Leu Gly Leu Arg Gly
500 505 510

Arg Arg Thr Leu Leu Val Val Thr His Arg Pro Ala Leu Ala Arg Gln
515 520 525

Ala Asp Gln Val Leu Leu Leu Glu Glu Gly Arg Leu Arg Leu Ser Gly
530 535 540

Leu His Ala Asp Leu Leu Val Arg Asp Asp Trp Tyr Ala Gly Phe Val
545 550 555 560

Gly Leu Ala Gly Glu Glu Ser Ser Ala Thr Val Val Asp Arg
565 570

<210> 37
<211> 558
<212> DNA
<213> Pseudomonas aeruginosa

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<220>
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<400> 37
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gatcgggcct tgatgttacc cgagagcttg gcacccagcc tgcgcgagca gggnnaattg 180

atccggtgga tgacctttg aatgaccttt aatagattat attactaatt aattggggac 240

cctanaggtc ccctttttta ttttaaaaat tttttcacaa aacggtttat ttncataaag 300

cttgctcaat caatcaccnt atccncggga attcggccta ggcggccaga tctgatcaag 360

agacagacct ccagctttgc atccggagcg accacacgag cgaggtcagt cactttcatc 420

gaaggaattt tcttgacata gatctcacca ccttccatgt cctcaaaggc atgccacact 480

aactcgacgc cctcctccaa agaaatcatg aaccgggtca tccgctcatc agtgataggc 540

aagacgccct tgtccttg 558

<210> 38
<211> 479
<212> DNA
<213> Klebsiella sp.

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gacttcaccg atactgtaaa acgccatagc agcctcacat caacctgata ccttaatacc 180

taaactaacg aattcaggca tcctgtacaa ctctattttc ttgtacagat aaagatatca 240

ggttgcggct cacagcgccc gggaaaaaag atgaaaaaat gtttagctga tttcgcggtg 300

gttcattttt tctccggcca tgcgacggcg ggtaggcccc ccaggcgcgc gctggcgaac 360

aaattgccct gaaactgtga ataccggct gattccagcc acatccactc ttcagcacgc 420

tcaacgccga cggctgagac cgcaatctcc agagaagtac agcatttgat aatcgcctg 479

<210> 39
<211> 516
<212> DNA
<213> Klebsiella sp.

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cgtctggttc gccctgagac ccgcgtggtg ttcctcgaat cgcccggctc gatcaccatg 180

gaagtgcacg atgtgccggc gatagtcgcc gccgtgcgtc aggtcgcccc ggaagcgatt 240

atcatgatcg ataacacctg ggcggcgggg atcctgttta aagccctgga ttttggcatt 300

gatatttcca ttcaggcagg caccaaatac ctgatcggcc attccgacgc catggtgggc 360

accgcggtgg cgaacgcgcg ctgctggccg cagctgcgtg aaaatgccta cctgatgggg 420

caaatgctgg acgccgatac tgcctatatg accagccgcg gcctgcgaac cctgggcgtg 480

cgcctgcgtc agcatcatga aagcagcctg cgcatc 516

<210> 40
<211> 377
<212> DNA
<213> Klebsiella sp.

<400> 40
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cccgcagcgt gtggcccagg agatgcaaaa agagattgcc atcatcctgc agcgtgaaat 120

taaagatccg cgtctgggca tgatgaccac cgtttccggt gtggaaatgt cccgtgacct 180

ggcctatgcc aaggtgtatg tcaccttcct taacgacaaa gatgaagccg cggtgaaagc 240

gggcatcaaa gcgctgcagg aagcttctgg ctttatccgc tctctgctgg ggaaagcgat 300

gcgtctgcgc atcgtaccgg aactgacttt cttctacgac aactcactgg tggaagggat 360

gcgtatgtcc aacctgg 377

<210> 41
<211> 625
<212> DNA
<213> Klebsiella sp.

<400> 41
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gcgctgatct gccgcggcga aaagctctcc atcgccatca tggcgggtct gctggaagcc 180

cgtggacaca aagtcagtgt cattaacccg gtcgaaaaac tgctcgccgt gggtcactat 240

ctggaatcca ccgtcgatat cgccgaatcc acccgccgca ttgccgccag ccagatcccg 300

gcagaccata tgatcctgat ggccgggttt accgccggca atgagaaagg cgagctggtg 360

gtgctggggc gtaacggctc cgactactcg gctgcggtac tggccgcctg cctgcgcgct 420

gactgctgcg aaatctggac cgatgtcgac ggagtgtaca cctgcgatcc gcgtcaggtg 480

ccggatgcgc gcctgctgaa atcgatgtct tatcaggagg cgatggagct ctcctacttt 540

ggcgcgaaag tgctgcaccc gcgcaccatt gcccctatcg cccagttcca aatcccatgc 600

ctgattaaaa ataccggcaa ccccc 625

<210> 42
<211> 355
<212> DNA
<213> Klebsiella sp.

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tcaccagcgg ctgggttttc agatactcaa cgatcgccag ggcatttcgc tgcgccactt 180

ccatccgtgg agacagcgtc cgcagcccgc gcaacagcag atagctgtcg aaggcgctgc 240

cggtgacgcc aatattattc gcccaccatg ccagttcggt gacagttgcc ggatctttgg 300

caatcaccac cccggccacc acatcggagt gaccattgag gtatttggta cagga 355

<210> 43
<211> 500
<212> DNA
<213> Klebsiella sp.

<400> 43
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gctggtgacc ggcgtcggct gatggtgagc gaacagcttc tcgcccgctt ccagctcgtc 180

gaagacgctc tccatcatgc ggtcatgcag ctccgccgcc accgcggccc actgcgcttc 240

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cagaccgcag ttgtgagcga tatcggtagc tttagaagac cagggagaga tggtgccagg 360

gcgaggggtc acgagcagta atttaccggt cggggtatgg ctgcttaagc tcgggccata 420

ctgaagcagt cgcgccaggc gctcgcgatc gtcagcgctc agcggggcgt tcagatcggc 480

aaaatgaata tattcggcat 500

<210> 44
<211> 439
<212> DNA
<213> Klebsiella sp.

<400> 44
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gaataagtcc ggccggaaaa tcagcatagc gtgagtgcgg ggccaggaaa gagtcgtcga 180

aaccgcgggt cagtaaggcg tgcggatgaa gaatatggtg ttcatagacg ccggaaatct 240

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aacagacgaa cagcgtcgaa gtgacgtgat ccttggccca ctccagcacc tgtttgatct 360

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ggccgtcaaa gttctgatc 439

<210> 45
<211> 297
<212> DNA
<213> Klebsiella sp.

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gcgtgggcgc tggaaaatct gccgggaaac tatgtgctgt cgtcgagctt tggcattcag 180

gcggcggtaa gtttgcatct ggtgaatcag atccgcccgg acattccggt gatcctcacc 240

gataccggct acctgttccc ggaaacctat cagtttattg acgagctgac ggacaag 297

<210> 46
<211> 502
<212> DNA
<213> Klebsiella sp.

<400> 46
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acctgcccta ccgtcaggtc ggtgtggtgc tgggcaccgc caaatattac cgcaccggcg 180

tcatcaatca gtattaccgt taccgcatcc agggtgcgct gaacgcctac aacagcggca 240

aggtcaacta tctcctgctg agcggcgata atgctctgca aagctacaat gaaccgatga 300

ccatgcgtcg ggacctgatt aaaggcggcg tcgatcccgc ggatatcgta ctggactatg 360

ccggtttccg taccctcgac tcgatcgtcc gtacccggaa agtgttcgac accaacgact 420

tcattatcat cacccagcgc ttccactgcg aacgggcgct gtttatcgcc ctgcatatgg 480

ggatccaggc ccagtgctac gc 502

<210> 47
<211> 500
<212> DNA

<213> Klebsiella sp.

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gatccgctca aacagctgca ggccgagcac cttctcaaag cgcgccagct cgcggctgac 120

cgtgggttgc gaggtgtgca gcatccgcgc cgcttcggtc aggttgccgg tggtcatcac 180

cgcgtgaaag atttcgatat gacgcaaatt gacggctggc atgcggtctc cgtgaggctc 240

ggctggaacc atatcatttt tgcatagagt cgcgataaaa cgatattttt tattcgtctg 300

tcactgtggc gtaatcagaa aaaacagcga ccaacacacg cactgcaccg gagttcttat 360

gccacactcg ctttacgcca ccgatactga cctgaccgcg gacaacctgc tgcgcctgcc 420

ggcggaattt ggctgcccgg tctgggtcta tgatgcgcag attattcgcc gccagatagc 480

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<210> 48
<211> 229
<212> DNA
<213> Klebsiella sp.

<400> 48
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accctcttgc ccgctaagtg cggtcactct gtcataggcc gcgccgctgc tgcagcacat 120

ccagtacctg ctgagcgtta gctttcagat cttcatgccc gtgtaaacgc atcaatatgg 180

cgacgttggc ggcgacggcg gcttcgtgag cggcttcacc tttaccttg 229

<210> 49
<211> 466
<212> DNA
<213> Klebsiella sp.

<400> 49
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gcctttctta acgatattca gccacggccc ttcgagatgc aggcccagcg cctggttcgg 180

atgtttttgc agatattcgc gcatcacgcg cacgccttgc ttcatcagat cgtcgctgga 240

ggtaatcagc gtcggcagga agctggtgca gcctgagcgt tcgttggcct tctgcatgat 300

ctccagcgtt tcgacagtga ccgcctctgg gctgtcgtta aactgcacgc cgccgcagcc 360

gttgagctgg acgtcgataa aaccgggggc gattattgcg ccgttgactg agcgctgctc 420

gatgtcagac ggcaaatctg ccagcggaca aagacgttcg ataaag 466

<210> 50
<211> 450
<212> DNA
<213> Klebsiella sp.

<400> 50
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atcggggttg gctgcgagca tatcccgggt ctcttcatac aacaggacat ccacgctggc 180

ggcggggtac tgctgtttca gcgcgtgaat aagcggcgtg atcagcagca tgtcgccatg 240

atggcgcagc ttaatgacca ggatccgcgc cgggttcaac gggccgcggg agagggtttc 300

aggcgtcata ctctgttctt catccaggat aagggttccg attctagggg atcagacaga 360

ttgagagaag cgttgtattg ctctaccatg acccgatacg tatggcctga ggacgttttc 420

gtgcacaatc ccgcaatttc tcatcacgat 450

<210> 51
<211> 450
<212> DNA
<213> Klebsiella sp.

<400> 51
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cttgctggct catggtttgg atccttagtc tgtgtcctgg cgccttgttg acgagcataa 120

aaaaacccgc gccaaggcgc gggttttata gtcttgctgg aagatgactt aacgctgaac 180

gtcgcccaac agcctaccga gcaaatggca tgcgtttagt agtagtaggc tggtgatacg 240

agcggtgcga atcattgcgt caaactccag atgaaatcgt tatgctttta gagttactgg 300

atagccgttt taaagtcaac ccctggcatg gaaaaagcgt tttgggctga ctaaatgaat 360

tagcaaaatg tgctgatgta agccccattt tgccgaagat cctattttgg accgaaggcg 420

gtttatcccc aatttgtttc atttgaaaaa 450

<210> 52
<211> 575
<212> DNA
<213> Klebsiella sp.

<400> 52
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gccgaggtca aaccggagca ggtgctggtc agccgcggcg ccgacgaagg catcgagctg 120

ctgatccgcg ccttctgtga gcccggcgaa gacgcggtgc tctactgccc gccgacctac 180

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ctgctggaga tgacccgcgg caaagccatc gtggtggccg acgaagccta tattgaattc 420

tgcccgcagg cgacgctcgc cggctggctc agcgactatc cgcacctggt ggtgctgcgc 480

acgctgtcca aagccttcgc cctcgccggc ctgcgctgcg gcttcaccct cgccaacgcc 540

gaggtgatta acgtgctgct gaaagtgatc gcccc 575

<210> 53
<211> 375
<212> DNA
<213> Klebsiella sp.

<400> 53
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tttaaataga cttctgccgt tttcaatgct tcggcgatgg tcacatccat atcaaggtaa 120

cggtaggttc caagacgacc gacaaaagtg atgttggttt cattctcggc caatgacaaa 180

tatttttcaa gaagagccat ttctcccatc tggcgaatag gatagtaagg aatatcattt 240

tcttcacaag cacggctata ctctttataa caaacagagc cgtcgtgttg ttcccaggga 300

gaaaaatatt tatgttcagt gatgcgagta tagggcacat ccacagaaca gtagttcatc 360

actgcgcatc cctgg 375

<210> 54
<211> 400
<212> DNA
<213> Klebsiella sp.

<400> 54
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acaatccgct agcgagtatg attcttagtt ggcgtgattt attcatgaat gggactctta 120

attttgagta tatttctata ctctatttta cgggaattat tttgacggtt gtcggtttgt 180

ctattttcaa taaattaaaa tatcgatttg cagagatcta aaagtgcgct ataagagcag 240

catgctaggc tatttatggt cagtagcaaa tccattgctt tttgccatga tttactattt 300

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cttgtttccg tggcaatggt ttgccagttc ggccactaac 400

<210> 55
<211> 413
<212> DNA
<213> Klebsiella sp.

<400> 55
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ggctcgaggt tatagctggt gccatgatag cgctgatgac ggacgttctg ctcttcgacc 120

ttggcggcga agaacttttc cgatggccag aagccgtcgc taaaaatatg tttttgcagt 180

tcaaggaaca gcgcgacgtc gccgatcagc aggcgcgatt cgattaagtt ggtggcaacg 240

gtcagatccg agagaccttc cagcaggcac tcttcgaggg tgcgtacgct gtggcccacc 300

tccagcttga cgtcccacag cagggtgagc agttcgccga ctttttgcgc ctggtcgtcc 360

ggcagttttt tacgactgag gatcagcaga tcgacgtctg agagcgggtg cag 413

<210> 56
<211> 500
<212> DNA
<213> Klebsiella sp.

<400> 56
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ccggtgctgg aagagatgcg cgcaaagggg atgaacctca gcggtccgct gccggcagac 120

actctctttc agccgaaata tcttgatcat gccgatgcgg tactcgcgat gtaccacgat 180

cagggcctgc ccgtgctaaa ataccagggc tttggccgcg gcgtgaacat tacgctcggt 240

ttacctttta ttcgtacctc cgtcgaccac ggcaccgcac tggaattagc gggccaggga 300

aaagcggacg tcggcagttt tatcacggcg cttaatctcg ccatcaaaat gattgttaat 360

acccaatgaa taatcgagtc catcagggcc atttagcccg caaacgcttc gggcagaact 420

tcctcaacga tcagtttgtg atcgacagca tcgtctcggc gattaacccg cagaaaggcc 480

aggcgatggt tgaaatcggc 500

<210> 57
<211> 473
<212> DNA
<213> Klebsiella sp.

<400> 57
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ggaagaagtt tgcgcacgtc agatcgacgc cgtgctgaaa acccagggcg ctgccgcttt 120

cgaaggcgtg gttatcgctt acgaaccagt atgggctatc ggtaccggca aatcagcgac 180

cccggctcag gcgcaggcgg tgcacaaatt catccgtgac cacattgcta aagctgacgc 240

caaaatcgct gagcaagtga tcatccagta cggcggttcc gttaacgctg gcaacgccgc 300

agagctgttc acccagccgg acatcgacgg cgcgctggtt ggcggcgcct ccctgaaagc 360

tgacgctttc gcggtgatcg ttaaagcagc agaagcagcg aaaaaagcgt aattcgcttt 420

tcccggtggc gacacgcgac cgggttgact gacaaaacgt gggagcccgg cct 473

<210> 58
<211> 463
<212> DNA
<213> Klebsiella sp.

<400> 58
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taatttttgt gtacgctctg acgagcgcac aataaaacaa gacgaatttt tgaacaattg 120

tctttaaatt tgttaattga attgatctgt tgttgtttaa aggtatttga atttcttttg 180

tatagatatg taaattaaca ttgaaaagcc atttcaaaaa ttaaatatat ggcgaacata 240

gctattaact tatagttaac atcttcccgg gttgcctttt gatacttcgg gtaatatatt 300

tatttcgcac atcaaaataa ctctttttttc ttctgtttgt tattcatggc catctattgg 360

cgaaataagg cagagtagag ggggatgtgc ctaatatcct gcggaaggaa cgcaatgtac 420

atttacaggg aggagctgac gagccgtttc gcgatagctt tag 463

<210> 59
<211> 526
<212> DNA
<213> Klebsiella sp.

<400> 59
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gaagagtatt ttcttctgac agcatgcctt taaaattatt gcggcagttt actattgctg 120

catataaata tattgccagt aataagcgct gtatatttat gtttgaacat gaccgcgaca 180

gaaaaaaact ggctaagttg gttggactcg aagaacaaca gactattgtt attgatggtg 240

caggcattaa tccagagata tacaaatatt ctcttgaaca ggatcacgat gtccctgttg 300

tattgtttgc cagccgtatg ttgtggagta aaggactggg cgacttaatt gaagcgaaga 360

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atgataaaga tgcaatttcc cttcagggtc attgaaaatt ggcatcagca aggattaatt 480

aactggttag gtcgttcgaa taatgtttgc gatcttattg agcaat 526

<210> 60
<211> 473
<212> DNA
<213> Klebsiella sp.

<400> 60
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gattgctgaa cgtaagatca agttcctgct gcgcgcccag gcgcaggtgc aggtggtcgc 120

tgaaacgctg tcaccggcgc tggccgatct ggctgcgcgc caggcactca gctggcgggc 180

gacggcattc agcgactcgc tggtggatga tgtctttctg gtgattgcgg ccaccgagga 240

tgaggcgctt aaccagcggg tgtttgcggc agctaacgcg cgctaccggt tggtcaacgt 300

ggtggataac caggcgctgt gctcgtttgt tttcccttct atcgtcgacc gttcgccgct 360

gctggtggcg atctcctcca gcggtaaagc gccggtgttg tcgcgcattc tgcgtgaaaa 420

aatcgaagcg ctgctgccga cgaatctcgg tcggctggcg gaatcagcaa gct 473

<210> 61
<211> 451
<212> DNA
<213> Klebsiella sp.

<400> 61
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cattctaaca gcagcattca gaggggcaat gattttgggc aaccgattac gacgatcgcc 120

gcaaatgcta aaaaagggag aggggattac cagctggcgg gcttttccgc gccgagatta 180

tccagcacgg cgcgcagcgc caggccgtca ggaaagtgaa ggtccggggc gatctcgaac 240

agcggccaga gcataaagcc gcggtttttc atatcgtagt gcggaacggt caggcgctcg 300

ctgttaatga cagcatcgcc aaacagcatg atatcgaggt ccagcgtgcg cggcccccag 360

cgttcggctt tgcgcactcg cccctgctgc agttcgatgc gctgagtatg atcgagcagc 420

gtctcggggg gcagggcggt ttccagcgca a 451

<210> 62
<211> 525
<212> DNA
<213> Klebsiella sp.

<400> 62
ggcttaacgc cagctatgtc aacgctgcgg ttatgcggat ttttcatgcc tctgcggcta 60

acagaaaaaa gccttatgat agctatacta atggggcttt ttactccgtt ttgacccgat 120

tcctgaccgg cgtcagggtc aagtcacaaa aatcatcaca attttccgtc accggcgcta 180

caatcgaccg aagtcacaat ctcaaatcag aagagtattg ctaatgaaaa acatcaaccc 240

aacgcagacc tctgcctggc aggcattaca gaaacacttc gacgaaatga aagatgtcac 300

tatcagcgag cttttcgcca aagatagcga ccgtttttct aaattttccg cgacgttcga 360

cgatctgatg ctggtggact tctccaaaaa ccgcatcact gaagagacgc tggctaaact 420

gcaggatctg gcgaaagaga ctgacctggc gggcgctatc aagtcgatgt tctcaggtga 480

gaagatcaac cgcaccgaag accgcgcggt actgcacgtc gcgct 525

<210> 63
<211> 475
<212> DNA
<213> Klebsiella sp.

<400> 63
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aagattcgca gtaaaactcg gcgttttgcg ccttctcggc gaaatgatag agctcagctt 420

cggggaaata gggcttttta taacggccaa acggcacatt gaactcgccg cgcag 475

<210> 64
<211> 286
<212> DNA
<213> Klebsiella sp.

<400> 64
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cctgcgataa cagcgattca aaagcgccaa ccgttggcgc agcagcggag agcaatgcca 120

gcggccaggc aatcagcctg ctggatggca agctgagctt caccctgcct gcgggcatgg 180

ccgaccagag cggcaaactg ggtacccagg cgaacaatat gcacgtctac tctgacgcta 240

ccggccagaa agcggtcatc gtcatcgtcg gcgacagcac caatga 286